

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:26:32 : Search time 1840 Seconds  
(Without alignments)  
807.491 Million cell updates/sec

Title: US-09-626-616-7\_COPY\_354\_424

Perfect score: 71

Sequence: 1 GCACCTGTCGACCCATGC.....ACAGCTGTCCTCGACC 71

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3020346

Minimum DB seq length: 35

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

GenBank: \*  
1: gb\_ba: \*  
2: gb\_hlg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vi: \*  
30: em\_hlg\_hum: \*  
31: em\_hlg\_inv: \*  
32: em\_hlg\_other: \*  
33: em\_hlggo\_inv: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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1	71	100.0	305	9	HSOPRM11	AF024515 Homo sapi
2	71	100.0	520	11	G53082	G53082 SHGC-84785
3	71	100.0	1203	9	AF286024	AF286024 Macaca mu
4	71	100.0	1399	9	AY038989	AY038989 Macaca fa
5	71	100.0	1610	6	ARI06017	ARI06017 Sequence
6	71	100.0	1610	9	HUMOP10IDA	L129301 Homo sapien
7	71	100.0	96310	9	AL136444	AL136444 Human DNA
8	71	100.0	182048	2	AC027439	AC027439 Homo sapi
9	71	100.0	182383	2	AC021745	AC021745 Homo sapi
10	69.4	97.7	1182	6	AX280923	AX280923 Sequence
11	69.4	97.7	1203	6	AX280921	AX280921 Sequence
12	69.4	97.7	2160	6	ARI162044	ARI162044 Sequence
13	69.4	97.7	2162	6	A87781	A87781 Sequence 7
14	69.4	97.7	2162	9	HUMOR1X	L25119 Human Mu op
15	67.8	95.5	1473	9	HSU12569	U12569 Human mu op
16	63	88.7	1881	4	PIGMOOPR	I38645 Sus scrofa
17	61.4	86.5	1415	4	BT089677	BT089677 Bos taurus
18	56.6	79.7	1334	10	AF074973	AF074973 Mus musc
19	56.6	79.7	1346	10	AF167566	AF167566 Mus musc
20	56.6	79.7	1365	10	AF167565	AF167565 Mus musc
21	56.6	79.7	1367	10	RNI35424	U35424 Rattus norv
22	56.6	79.7	1401	10	RATMOP10ID	L22455 Rat mu opio
23	56.6	79.7	1423	10	AF062753	AF062753 Mus musc
24	56.6	79.7	1440	10	AF260306	AF260306 Mus musc
25	56.6	79.7	1440	10	AF400246	AF400246 Mus musc
26	56.6	79.7	1448	10	RNI02083	U02083 Rattus norv
27	56.6	79.7	1543	10	AF074974	AF074974 Mus musc
28	56.6	79.7	1569	10	AF260308	AF260308 Mus musc
29	56.6	79.7	1569	10	AF400248	AF400248 Mus musc
30	56.6	79.7	1586	10	RATMORA	L13069 Rattus norv
31	56.6	79.7	1610	10	MMU26915	U26915 Mus muscu
32	56.6	79.7	1614	10	AF260307	AF260307 Mus muscu
33	56.6	79.7	1614	10	AF400247	AF400247 Mus muscu
34	56.6	79.7	1618	6	ARI06013	ARI06013 Sequence
35	56.6	79.7	1618	6	ARI06014	ARI06014 Sequence
36	56.6	79.7	1618	6	ARI53354	ARI53354 Sequence
37	56.6	79.7	1618	6	ARI53355	ARI53355 Sequence
38	56.6	79.7	1729	10	AF167568	AF167568 Mus musc
39	56.6	79.7	1944	10	S79903	S79903 mu oploid
40	56.6	79.7	2045	10	AF167567	AF167567 Mus musc
41	56.6	79.7	2093	10	MMORI	U10558 Mus muscu
42	56.6	79.7	2135	6	ARI48257	ARI48257 Sequence
43	56.6	79.7	2135	10	RATMORA1A	L20684 Rattus norv
44	56.6	79.7	2137	10	AB047546	AB047546 Mus musc
45	56.6	79.7	2229	6	A68824	A68824 Sequence 1
46	56.6	79.7	2229	6	MMU19380	U19380 Mus muscu
47	56.6	79.7	2397	10	RATROB	D16349 Rat mRNA f
48	56.6	79.7	2397	10	RATROB	AC055776 Mus muscu
49	49.2	69.3	6494	6	AX346295	AX346295 Sequence
50	49.2	69.3	6494	6	AX348524	AX348524 Sequence
51	37.4	52.7	6494	6	AX346294	AX346294 Sequence
52	37.4	52.7	6494	6	AX348523	AX348523 Sequence
53	28	39.4	73972	2	AC100554	AC100554 Mus muscu
54	28	39.4	161023	2	AC069508	AC069508 Homo sapi
55	28	39.4	180223	9	AC062017	AC062017 Homo sapi
56	27.2	38.3	135666	2	AL513013	AL513013 Homo sapi
57	26.8	37.7	110551	2	AC103091	AC103091 Rattus nor
58	26.8	37.7	119048	2	AP004167	AP004167 Oryza sat
59	26.8	37.7	234777	2	AL670236	AL670236 Mus muscu
60	26.8	37.7	253111	2	AL627204	AL627204 Mus muscu
61	26.8	37.7	254197	2	AF389853	AF389853 Mus muscu
62	26.6	37.5	2051	3	DSU32096	U32096 Drosophila
63	26.6	37.5	10647	1	AE002031	AE002031 Deinococc
64	26.6	37.5	134914	9	AC004542	AC004542 Homo sapi
65	26.6	37.5	217292	9	AF288742	AF288742 Homo sapi
66	26.4	37.2	109519	6	AX195929	AX195929 Sequence
67	26.4	37.2	124669	2	AP004325	AP004325 Oryza sat
68	26.4	37.2	159218	2	AL450307	AL450307 Homo sapi
69	26.2	36.9	785	1	AF338352	AF338352 Cellulomo
70	26.2	36.9	785	9	HSA331011	AJ331011 Homo sapi
71	26.2	36.9	836	9	HSA342700	AJ342700 Homo sapi
72	26	36.6	10314	1	AE004600	AE004600 Pseudomon
73	26	36.6	10964	1	AE004892	AE004892 Pseudomon

74	26	36.6	42704	1	SCBAC17A6	AL566248	Streptomy	c 147	25	35.2	193382	2	AC021583	AC021583	Homo sapi
75	26	36.6	70282	2	AP001505	AP001505	Homo sapi	c 148	25	35.2	196612	9	AC021582	AC021582	Homo sapi
76	26	36.6	110000	2	AC091288_1	Continfection (2 of	c 149	25	35.2	212459	9	AC069562	AC069562	Mus muscu	
77	26	36.6	110000	2	AC091288_2	Continfection (3 of	c 150	25	35.2	212459	10	AC026385	AC026385	Mus muscu	
78	26	36.6	120598	2	OSJN00104	AL606653	Oryza sat	c 151	25	35.2	325600	10	RME603644	AL603644	Rhizobium
79	26	36.6	158456	9	CNS01DXB	AL139194	Human chr	c 152	24.8	34.9	10722	33	AC050963	AC050963	Giardia 1
80	26	36.6	194523	9	HS323MR2	AL022476	Human DNA	c 153	24.8	34.9	2190	6	AX014151	AX014151	Sequence
81	26	36.6	204177	2	AC008761	AC008761	Homo sapi	c 154	24.8	34.9	2281	9	AK025719	AK025719	Homo sapi
82	26	36.6	223169	2	AC091248	AC091248	Homo sapi	c 155	24.8	34.9	4156	9	HSIGF27	HSIGF27	Human DNA f
83	26	36.6	276261	2	HSAC000406	AC000406	Homo sapi	c 156	24.8	34.9	12234	1	AB070953	AB070953	Streptomy
84	26	36.6	340000	9	HS21C101	AL163301	Homo sapi	c 157	24.8	34.9	39210	9	HSE118G4	HSE118G4	Human DNA s
85	26	36.3	12299	1	AE006000	AE006000	Caulobact	c 158	24.8	34.9	50508	9	AC004940	AC004940	Homo sapi
86	25.8	36.3	12497	1	AE004691	AE004691	Pseudomon	c 159	24.8	34.9	78505	2	AC006408	AC006408	Homo sapi
87	25.8	36.3	39741	1	SC8E7	AL331338	Streptomy	c 160	24.8	34.9	100785	9	AP000617	AP000617	Homo sapi
88	25.8	36.3	52173	9	HS66PDGEN	X55448	H. sapliens G	c 161	24.8	34.9	123551	2	AC005809	AC005809	Homo sapi
89	25.8	36.3	121949	2	AP004190	AP004190	Oryza sat	c 162	24.8	34.9	131274	2	AC069506	AC069506	Homo sapi
90	25.8	36.3	159744	2	AP003892	AP003892	Oryza sat	c 163	24.8	34.9	137371	2	AC044908	AC044908	Homo sapi
91	25.8	36.3	219447	9	HUMFING6PD	LA4140	Homo sapien	c 164	24.8	34.9	138094	2	AC009417	AC009417	Homo sapi
92	25.8	36.3	346510	1	AP003011	AP003011	Mesorhizo	c 165	24.8	34.9	149628	2	AC034128	AC034128	Homo sapi
93	25.6	36.1	1865	9	HSA131613	AJ131613	Homo sapi	c 166	24.8	34.9	156255	2	AC092903	AC092903	Homo sapi
94	25.6	36.1	1967	9	BC015797	BC015797	Homo sapi	c 167	24.8	34.9	156879	2	AC026857	AC026857	Homo sapi
95	25.6	36.1	1969	9	BC007355	BC007355	Homo sapi	c 168	24.8	34.9	157048	9	AC067744	AC067744	Homo sapi
96	25.6	36.1	2004	6	AX061232	AX061232	Sequence	c 169	24.8	34.9	159129	30	AC023246	AC023246	Homo sapi
97	25.6	36.1	8626	9	HSA131612	AJ131612	Homo sapi	c 170	24.8	34.9	159409	2	AC092900	AC092900	Homo sapi
98	25.6	36.1	18577	9	HSA1	Z93437	Human DNA s	c 171	24.8	34.9	160877	2	AC026560	AC026560	Homo sapi
99	25.6	36.1	125630	2	AC090650	AC090650	Arabidops	c 172	24.8	34.9	163300	2	AC060820	AC060820	Homo sapi
100	25.6	36.1	156028	2	AC025684	AC025684	Homo sapi	c 173	24.8	34.9	165125	2	AC108064	AC108064	Homo sapi
101	25.6	36.1	160839	2	AC069257	AC069257	Homo sapi	c 174	24.8	34.9	165188	2	AP003716	AP003716	Homo sapi
102	25.6	36.1	173068	4	AC091660	AC091660	Bos tauri	c 175	24.8	34.9	166246	2	AF271408	AF271408	Homo sapi
103	25.4	35.8	551	2	HSA323418	AJ3323418	Homo sapi	c 176	24.8	34.9	171759	2	AC073650	AC073650	Homo sapi
104	25.4	35.8	55501	2	AC107984	AC107984	Homo sapi	c 177	24.8	34.9	183591	9	AC092051	AC092051	Homo sapi
105	25.4	35.8	66933	2	AC101755	AC101755	Mus muscu	c 178	24.8	34.9	191967	2	AC021962	AC021962	Homo sapi
106	25.4	35.8	68066	2	AC110285	AC110285	Homo sapi	c 179	24.8	34.9	200214	2	AL626775	AL626775	Mus muscu
107	25.4	35.8	110000	2	LMFCHR31_04	Continfection (5 of	c 180	24.8	34.9	216016	2	AL626775	AL626775	Mus muscu	
108	25.4	35.8	117026	9	HS329A5	Z97832	Human DNA s	c 181	24.8	34.9	338579	1	AP003004	AP003004	Mesorhizo
109	25.4	35.8	132070	9	AC003663	AC003663	Homo sapi	c 182	24.6	34.6	623	9	HSPRCSH10	HSPRCSH10	Human prote
110	25.4	35.8	154918	9	AL138781	AL138781	Human DNA	c 183	24.6	34.6	718	9	HSN337288	HSN337288	Homo sapi
111	25.4	35.8	175515	2	AC098128	AC098128	Rattus no	c 184	24.6	34.6	14439	1	AE004655	AE004655	Pseudomon
112	25.4	35.8	178073	1	SC0590464	AL590464	Streptomy	c 185	24.6	34.6	23786	9	HS415C1	HS415C1	Human DNA s
113	25.4	35.8	191222	2	AC027601	AC027601	Homo sapi	c 186	24.6	34.6	24790	1	AB070946	AB070946	Streptomy
114	25.4	35.8	201602	2	AC074146	AC074146	Mus muscu	c 187	24.6	34.6	35350	9	AF414442	AF414442	Homo sapi
115	25.4	35.8	204940	2	AC069007	AC069007	Homo sapi	c 188	24.6	34.6	39170	2	AC005202	AC005202	Homo sapi
116	25.4	35.8	204969	2	AC091132	AC091132	Homo sapi	c 189	24.6	34.6	40356	1	SC16	SC16	Streptomy
117	25.4	35.8	229482	2	AC074149	AC074149	Mus muscu	c 190	24.6	34.6	51920	2	CER08A5	CER08A5	Caenorhabdi
118	25.2	35.5	864	5	AC072353	AB072353	Aldabrach	c 191	24.6	34.6	86767	2	AC106263	AC106263	Rattus no
119	25.2	35.5	17856	1	SCR20	AL504057	Streptomy	c 192	24.6	34.6	92509	1	AL646086	AL646086	Rattus no
120	25.2	35.5	22134	1	SC152	AL505057	Streptomy	c 193	24.6	34.6	95280	9	AC073133	AC073133	Rattus no
121	25.2	35.5	34725	1	SC1B2	AL505057	Streptomy	c 194	24.6	34.6	98771	2	AC025044	AC025044	Oryza sat
122	25.2	35.5	44160	9	AC000049	AC000049	Homo sapi	c 195	24.6	34.6	111977	2	AP000717	AP000717	Homo sapi
123	25.2	35.5	60432	2	AC102080	AC102080	Mus muscu	c 196	24.6	34.6	123469	2	AC097087	AC097087	Rattus no
124	25.2	35.5	66400	2	AC105064	AC105064	Drosophill	c 197	24.6	34.6	133069	2	AC026836	AC026836	Homo sapi
125	25.2	35.5	118914	5	AC094011	AC094011	Gallus ga	c 198	24.6	34.6	133655	9	AL357274	AL357274	Human DNA
126	25.2	35.5	135509	8	AC037426	AC037426	Oryza sat	c 199	24.6	34.6	152397	8	AC027660	AC027660	Oryza sat
127	25.2	35.5	139726	2	AC096306	AC096306	Rattus no	c 200	24.6	34.6	157122	2	AC105491	AC105491	Rattus no
128	25.2	35.5	157533	9	AL354709	AL354709	Human DNA	c 201	24.6	34.6	157564	2	AC025996	AC025996	Homo sapi
129	25.2	35.5	163052	3	AC007472	AC007472	Drosophill	c 202	24.6	34.6	157762	9	AP001893	AP001893	Homo sapi
130	25.2	35.5	171491	2	AC022606	AC022606	Homo sapi	c 203	24.6	34.6	161610	2	AC011728	AC011728	Homo sapi
131	25.2	35.5	189370	1	AF010496	AF010496	Rhodobact	c 204	24.6	34.6	168995	2	AP002359	AP002359	Homo sapi
132	25.2	35.5	221372	2	AL390778	AL390778	Homo sapi	c 205	24.6	34.6	171179	2	AC034140	AC034140	Homo sapi
133	25.2	35.5	265387	3	AE003820	AE003820	Drosophill	c 206	24.6	34.6	180238	2	AC073688	AC073688	Mus muscu
134	25.2	35.5	349498	1	AP003002	AP003002	Mesorhizo	c 207	24.6	34.6	185324	2	AC026265	AC026265	Homo sapi
135	25	35.2	2042	3	DSU32097	U32097	Drosophilla	c 208	24.6	34.6	197126	2	AC023130	AC023130	Homo sapi
136	25	35.2	2056	3	DSU32095	U32095	Drosophilla	c 209	24.6	34.6	200920	2	AC069319	AC069319	Homo sapi
137	25	35.2	2057	3	DSU32094	U32094	Drosophilla	c 210	24.6	34.6	201380	2	AC092905	AC092905	Homo sapi
138	25	35.2	2069	3	DMU32091	U32091	Drosophilla	c 211	24.6	34.6	205317	9	AC093856	AC093856	Homo sapi
139	25	35.2	3759	9	AF153500	AF153500	Homo sapi	c 212	24.6	34.6	210827	2	AL626806	AL626806	Mus muscu
140	25	35.2	5931	1	SC146	AL499607	Streptomy	c 213	24.6	34.6	260418	2	AE006463	AE006463	Homo sapi
141	25	35.2	34962	1	SCG20A	AL360055	Streptomy	c 214	24.6	34.6	260967	2	AC091771	AC091771	Mus muscu
142	25	35.2	43147	1	SC4A10	AL109663	Streptomy	c 215	24.4	34.4	3527	1	SHU51222	SHU51222	Streptomyce
143	25	35.2	143291	9	HS163G9	AL108733	Human DNA	c 216	24.4	34.4	4171	1	MLUDNAA	MLUDNAA	M.luteus ri
144	25	35.2	159702	9	AL356433	AL356433	Human DNA	c 217	24.4	34.4	14980	1	SC4A9	SC4A9	Streptomy
145	25	35.2	166206	2	AC016927	AC016927	Homo sapi	c 218	24.4	34.4	71793	2	AC101733	AC101733	Mus muscu
146	25	35.2	172460	2	AC079798	AC079798	Homo sapi	c 219	24.4	34.4	78184	9	AC067722	AC067722	Homo sapi

C 220	24.4	34.4	79414	2	AC023502	Homo sapi	293	24	33.8	3274	1	AB020341
C 221	24.4	34.4	104228	2	AL354751	Human DNA	294	24	33.8	3387	6	AX235185
C 222	24.4	34.4	110000	2	AC107387_2	Continuation (3 of	295	24	33.8	3810	6	AK000048
C 223	24.4	34.4	122436	10	AB051897	Mus muscu	296	24	33.8	3900	6	AX235183
C 224	24.4	34.4	148348	2	AC104074	Homo sapi	297	24	33.8	7291	1	AE009865
C 225	24.4	34.4	154732	2	AC023236	Homo sapi	298	24	33.8	11103	1	AE004774
C 226	24.4	34.4	160682	2	AC099675	Homo sapi	299	24	33.8	12152	6	AX196110
C 227	24.4	34.4	164073	2	AC008032	Homo sapi	300	24	33.8	13345	1	AE004640
C 228	24.4	34.4	166181	9	HS37E16	Human DNA	301	24	33.8	15751	1	AF121000
C 229	24.4	34.4	174992	2	AC025822	Homo sapi	302	24	33.8	28106	1	DNAI1200
C 230	24.4	34.4	176543	2	AC025871	Homo sapi	303	24	33.8	32360	1	DNABRL01
C 231	24.4	34.4	178324	2	AC018828	Homo sapi	304	24	33.8	35101	1	AC005339
C 232	24.4	34.4	180629	2	AC104075	Homo sapi	305	24	33.8	36224	1	SC6E73
C 233	24.4	34.4	181210	9	AC011742	Homo sapi	306	24	33.8	42010	10	SCD78
C 234	24.4	34.4	188631	9	AC022383	Homo sapi	307	24	33.8	43872	10	AC002298
C 235	24.4	34.4	194070	2	AL663075	Mus muscu	308	24	33.8	47730	10	MMWHNGE
C 236	24.4	34.4	200050	1	AL646068	Rattus nor	309	24	33.8	75609	1	AL162416
C 237	24.4	34.4	202793	9	CNS06C83	Human chr	310	24	33.8	86896	1	RCU57682
C 238	24.4	34.4	210047	9	AC022384	AL591158	311	24	33.8	93172	2	AL357872
C 239	24.4	34.4	212855	2	AL596122	Mus muscu	312	24	33.8	93650	2	AL359635_4
C 240	24.4	34.4	216184	2	AC055773	Mus muscu	313	24	33.8	108930	2	AL513122
C 241	24.4	34.4	216381	2	AC011132	Homo sapi	314	24	33.8	110000	2	AL359635_3
C 242	24.4	34.4	217346	9	AC012363	Homo sapi	315	24	33.8	111977	2	AP000717
C 243	24.4	34.4	226758	9	AC006449	Homo sapi	316	24	33.8	115936	2	AL445205
C 244	24.4	34.4	322593	2	AC107084	Homo sapi	317	24	33.8	118183	2	AC090433
C 245	24.4	34.4	349116	1	AP003003	Mesorhizo	318	24	33.8	118313	9	AC003991
C 246	24.2	34.1	609	11	AU047620	Rattus no	319	24	33.8	130000	9	AC087259
C 247	24.2	34.1	677	8	AF261173	Saxifraga	320	24	33.8	139097	2	AC004591
C 248	24.2	34.1	1440	6	AF147705	Rhodobact	321	24	33.8	141469	9	AL139811
C 249	24.2	34.1	1782	6	AX103432	Sequence	322	24	33.8	143285	9	AL139423
C 250	24.2	34.1	1799	9	BC003533	Homo sapi	323	24	33.8	145063	2	AC027069
C 251	24.2	34.1	1804	6	AX355864	Sequence	324	24	33.8	151075	2	AC022594
C 252	24.2	34.1	1877	9	AK027669	Homo sapi	325	24	33.8	152129	2	AC027416
C 253	24.2	34.1	1944	6	AX103428	Sequence	326	24	33.8	155818	9	AC073504
C 254	24.2	34.1	2439	6	BC009383	Homo sapi	327	24	33.8	155885	9	AL442646
C 255	24.2	34.1	2439	6	AX059564	Sequence	328	24	33.8	155606	2	AC068038
C 256	24.2	34.1	2815	1	SLOCURS	X58793 S. lividans	329	24	33.8	157001	2	CNS07EP5
C 257	24.2	34.1	3167	1	AF019038	Pseudomon	330	24	33.8	157762	9	AP001893
C 258	24.2	34.1	5066	10	MMU132389	Mus muscu	331	24	33.8	158297	9	AC106779
C 259	24.2	34.1	8934	10	MUSB82R	L27595 Mus muscarl	332	24	33.8	158995	2	AL590679
C 260	24.2	34.1	10602	1	AE004874	Pseudomon	333	24	33.8	159748	2	AC016712
C 261	24.2	34.1	10850	1	SC2E9	AL021530 Streptomy	334	24	33.8	161610	9	AC011728
C 262	24.2	34.1	33311	9	AC004235	Homo sapi	335	24	33.8	162328	9	AP000350
C 263	24.2	34.1	43804	6	AG3469	Sequence 1	336	24	33.8	163144	2	AL365399
C 264	24.2	34.1	43804	6	A98892	Sequence 1	337	24	33.8	165190	2	AL162452
C 265	24.2	34.1	43804	14	AU046933	Avian adeno	338	24	33.8	168995	2	AP002359
C 266	24.2	34.1	52664	2	AC097284	Rattus no	339	24	33.8	169296	2	AC022198
C 267	24.2	34.1	57205	2	AC107995	Homo sapi	340	24	33.8	170114	2	AC016143
C 268	24.2	34.1	66948	2	AC100203	Mus muscu	341	24	33.8	171985	9	AL445675
C 269	24.2	34.1	147000	9	AP004242	Homo sapi	342	24	33.8	173025	9	CNS07TIV
C 270	24.2	34.1	152862	2	OSJN00168	Sequence	343	24	33.8	174764	9	AC108879
C 271	24.2	34.1	180341	2	AC094468	Rattus no	344	24	33.8	175562	2	AL139242
C 272	24.2	34.1	181339	9	AC027591	Homo sapi	345	24	33.8	176578	2	AC041008
C 273	24.2	34.1	183249	2	AC004828	Homo sapi	346	24	33.8	177156	2	AC106469
C 274	24.2	34.1	189344	2	AL627235	Mus muscu	347	24	33.8	177633	2	AC024098
C 275	24.2	34.1	192864	2	AC040981	Mus muscu	348	24	33.8	181029	30	AC026901
C 276	24.2	34.1	194296	9	AL354864	Human DNA	349	24	33.8	181175	9	AL138214
C 277	24.2	34.1	194622	2	AL645976	Mus muscu	350	24	33.8	182044	2	AL355872
C 278	24.2	34.1	199306	2	AC068459	Mus muscu	351	24	33.8	182108	2	AC091399
C 279	24.2	34.1	207184	2	AC020664	Homo sapi	352	24	33.8	182427	2	AL359749
C 280	24.2	34.1	303717	2	AC063930	Homo sapi	353	24	33.8	182422	2	AL356292
C 281	24.2	34.1	341887	1	AP003006	Mesorhizo	354	24	33.8	185324	2	AC026265
C 282	24.2	34.1	348077	1	AP003000	Mesorhizo	355	24	33.8	185978	2	AC097532
C 283	24.2	33.8	852	6	AX196125	Sequence	356	24	33.8	190599	9	AC009022
C 284	24.2	33.8	1113	1	AF090833	Streptomy	357	24	33.8	192550	2	AC025584
C 285	24.2	33.8	1415	9	HSGE13	Human gene	358	24	33.8	193168	2	AC011969
C 286	24.2	33.8	1524	6	AX106328	Sequence	359	24	33.8	193814	2	AL512326
C 287	24.2	33.8	1524	6	AX140619	Sequence	360	24	33.8	197019	9	AL157938
C 288	24.2	33.8	1524	6	AX200479	Sequence	361	24	33.8	198490	2	AC022983
C 289	24.2	33.8	1524	6	AX267135	Sequence	362	24	33.8	205414	2	AC027309
C 290	24.2	33.8	1548	6	AX018184	Sequence	363	24	33.8	208975	2	AC012465
C 291	24.2	33.8	2981	9	AK000235	Homo sapi	364	24	33.8	217238	2	AL591131
C 292	24.2	33.8	3115	1	DG1318781	Desulfovib	365	24	33.8	227482	2	AC008735
C 293	24.2	33.8	3274	1	AB020341	Desulfovib	293	24	33.8	3274	1	AB020341
C 294	24.2	33.8	3387	6	AX235185	Sequence	294	24	33.8	3387	6	AX235185
C 295	24.2	33.8	3810	6	AK000048	Homo sapi	295	24	33.8	3810	6	AK000048
C 296	24.2	33.8	3900	6	AX235183	Sequence	296	24	33.8	3900	6	AX235183
C 297	24.2	33.8	7291	1	AE009865	Alcaligenes	297	24	33.8	7291	1	AE009865
C 298	24.2	33.8	11103	1	AE004774	Pseudomon	298	24	33.8	11103	1	AE004774
C 299	24.2	33.8	12152	6	AX196110	Sequence	299	24	33.8	12152	6	AX196110
C 300	24.2	33.8	13345	1	AE004640	Pseudomon	300	24	33.8	13345	1	AE004640
C 301	24.2	33.8	15751	1	AF121000	Corynebact	301	24	33.8	15751	1	AF121000
C 302	24.2	33.8	28106	1	DNABRL01	Dictheobact	302	24	33.8	28106	1	DNABRL01
C 303	24.2	33.8	32360	1	AC005339	Homo sapi	303	24	33.8	32360	1	AC005339
C 304	24.2	33.8	35101	1	SC6E73	Streptomy	304	24	33.8	35101	1	SC6E73
C 305	24.2	33.8	36224	1	SCD78	Streptomy	305	24	33.8	36224	1	SCD78
C 306	24.2	33.8	42010	10	AC002298	Genomic s	306	24	33.8	42010	10	AC002298
C 307	24.2	33.8	43872	10	MMWHNGE	Human DNA	307	24	33.8	43872	10	MMWHNGE
C 308	24.2	33.8	47730	10	AL162416	M. musculus	308	24	33.8	47730	10	AL162416
C 309	24.2	33.8	75609	1	RCU57682	Human DNA	309	24	33.8	75609	1	RCU57682
C 310	24.2	33.8	86896	1	AL357872	Rhodobacter	310	24	33.8	86896	1	AL357872
C 311	24.2	33.8	93172	2	AL359635_4	Human DNA	311	24	33.8	93172	2	AL359635_4
C 312	24.2	33.8	108930	2	AL513122	Continuation (5 of	312	24	33.8	108930	2	AL513122
C 313	24.2	33.8	110000	2	AL359635_3	Continuation (4 of	313	24	33.8	110000	2	AL359635_3
C 314	24.2	33.8	111977	2	AP000717	Homo sapi	314	24	33.8	111977	2	AP000717
C 315	24.2	33.8	115936	2	AL445205	Human DNA	315	24	33.8	115936	2	AL445205
C 316	24.2	33.8	118183	2	AC090433	Chlamydom	316	24	33.8	118183	2	AC090433
C 317	24.2	33.8	118313	9	AC003991	Human BAC	317	24	33.8	118313	9	AC003991
C 318	24.2	33.8	130000	9	AC087259	Human sapi	318	24	33.8	130000	9	AC087259
C 319	24.2	33.8	139097	2	AC004591	Mus muscu	319	24	33.8	139097	2	AC004591
C 320	24.2	33.8	141469	9	AL139811	Human DNA	320	24	33.8	141469	9	AL139811
C 321	24.2	33.8	143285	9	AL139423	Human DNA	321	24	33.8	143285	9	AL139423
C 322	24.2	33.8	145063	2	AC027069	Homo sapi						

C 366	24	33.8	234381	2	AC074152	AC074152 Mus muscu	C 439	23.6	33.2	1110	4	SSFGDMR	X16638 Pig pgd mRNA
C 367	24	33.8	326249	2	AC034210	AC034210 Homo sapi	C 440	23.6	33.2	1124	11	G07120	G07120 human STS w
C 368	24	33.8	347660	1	AP002994	AP002994 Mesorhizo	C 441	23.6	33.2	1439	9	S71481S1	S71481S1 granuloocyte
C 369	24	33.8	347750	1	AP002998	AP002998 Mesorhizo	C 442	23.6	33.2	1540	1	REU83846	REU83846 Rhodococcus
C 370	23.8	33.5	553	1	MBMPB57	MBMPB57	C 443	23.6	33.2	1651	9	HUMIGR1PR	HUMIGR1PR Human insul
C 371	23.8	33.5	553	1	MBMPB57A	M35389 M.bovis Imm	C 444	23.6	33.2	1714	8	AIERG3	AIERG3 Human insul
C 372	23.8	33.5	553	6	E02260	E02260 DNA sequenc	C 445	23.6	33.2	1786	9	H0M1LGFIR	H0M1LGFIR Human insul
C 373	23.8	33.5	583	6	RABIGHVXO	M93185 Oryctolagus	C 446	23.6	33.2	2156	6	I58541	I58541 Sequence 1
C 374	23.8	33.5	597	6	AX073942	AX073942 Sequence	C 447	23.6	33.2	2156	6	HUMRANES	HUMRANES Human saplin
C 375	23.8	33.5	671	6	MSG10KAG	M25258 Mycobacteri	C 448	23.6	33.2	2156	9	HUMHMK145	HUMHMK145 Human saplin
C 376	23.8	33.5	914	1	MTBCGA	X13739 Mycobacteri	C 449	23.6	33.2	2214	9	HUMHMK145	HUMHMK145 Human saplin
C 377	23.8	33.5	1005	5	FUNLACDK	L23793 Fundulus he	C 450	23.6	33.2	4086	9	GGA291729	GGA291729 Gallus ga
C 378	23.8	33.5	1965	5	AK024529	AK024529 Homo sapi	C 451	23.6	33.2	4993	1	TA4HCCAR	TA4HCCAR Thauera a
C 379	23.8	33.5	2181	6	AR103051	AR103051 Sequence	C 452	23.6	33.2	11639	1	SCBACB81	SCBACB81 Arabidops
C 380	23.8	33.5	2376	6	AX001334	AX001334 Sequence	C 453	23.6	33.2	16405	1	AB041030	AB041030 Arthrobac
C 381	23.8	33.5	2376	10	MMSOX1	X94126 M. musculus	C 454	23.6	33.2	25342	9	AL157892	AL157892 Human DNA
C 382	23.8	33.5	2987	1	MTCEOBOP	X60352 M. tuberculosis	C 455	23.6	33.2	36368	1	SC9B5	SC9B5 Streptomy
C 383	23.8	33.5	3025	1	CHFRFA2A1	D10875 Gallus gall	C 456	23.6	33.2	49736	1	AF319998	AF319998 Stigmatal
C 384	23.8	33.5	3175	1	RM019726	U19726 Rhizobium m	C 457	23.6	33.2	67945	2	AC104887	AC104887 Mus muscu
C 385	23.8	33.5	4300	1	BP012276	U12276 Bordetella	C 458	23.6	33.2	69104	2	AC096014	AC096014 Rattus no
C 386	23.8	33.5	9004	1	SM059239	U59239 Seirratia ma	C 459	23.6	33.2	69683	2	AC106115	AC106115 Rattus no
C 387	23.8	33.5	10029	1	AE005310	AE005310 Escherich	C 460	23.6	33.2	72857	2	AC094297	AC094297 Rattus no
C 388	23.8	33.5	10401	1	AE004584	AE004584 Pseudomon	C 461	23.6	33.2	90225	2	AC020777	AC020777 Homo sapi
C 389	23.8	33.5	11519	1	AE004616	AE004616 Pseudomon	C 462	23.6	33.2	90325	9	AL591803	AL591803 Human DNA
C 390	23.8	33.5	12075	1	AE004641	AE004641 Pseudomon	C 463	23.6	33.2	96892	8	ATF148B	ATF148B Arabidops
C 391	23.8	33.5	12130	1	AE005133	AE005133 Halobacte	C 464	23.6	33.2	110467	8	AF381614	AF381614 Magnapor
C 392	23.8	33.5	12820	1	AE005273	AE005273 Escherich	C 465	23.6	33.2	114929	9	AC002401	AC002401 Homo sapi
C 393	23.8	33.5	13922	1	AE001894	AE001894 Deinococc	C 466	23.6	33.2	134594	2	AL358433	AL358433 Homo sapi
C 394	23.8	33.5	15372	1	AE007158	AE007158 Mycobacte	C 467	23.6	33.2	138168	2	AL445245	AL445245 Homo sapi
C 395	23.8	33.5	29699	4	SSRYRA	X69465 S. scrofa ge	C 468	23.6	33.2	139512	2	HSJ1169J3	HSJ1169J3 Human DNA
C 396	23.8	33.5	33818	1	MTCT78	Z77185 Mycobacteri	C 469	23.6	33.2	150594	2	AP000728	AP000728 Homo sapi
C 397	23.8	33.5	36277	9	AP000336	AP000336 Homo sapi	C 470	23.6	33.2	158052	9	AC027612	AC027612 Homo sapi
C 398	23.8	33.5	36583	1	SC5H1	AL049863 Streptomy	C 471	23.6	33.2	164059	2	AC106135	AC106135 Rattus no
C 399	23.8	33.5	55838	2	AC078792	AL078792 Homo sapi	C 472	23.6	33.2	164144	2	AC1012577	AC1012577 Homo sapi
C 400	23.8	33.5	58328	2	AC013967	AC013967 Drosophil	C 473	23.6	33.2	164715	2	AC096683	AC096683 Gallus ga
C 401	23.8	33.5	69221	2	AC103480	AC103480 Rattus no	C 474	23.6	33.2	165079	2	AC024517	AC024517 Homo sapi
C 402	23.8	33.5	84481	2	AL645728	AL645728 Homo sapi	C 475	23.6	33.2	166218	2	AC009293	AC009293 Homo sapi
C 403	23.8	33.5	89222	8	NCB1F11	AL670011 Neurospor	C 476	23.6	33.2	168558	9	AC006948	AC006948 Homo sapi
C 404	23.8	33.5	90763	8	NCB10H4	AL670010 Neurospor	C 477	23.6	33.2	171222	2	AC011825	AC011825 Homo sapi
C 405	23.8	33.5	100000	2	AP000215	AP000215 Homo sapi	C 478	23.6	33.2	175529	2	AL591916	AL591916 Homo sapi
C 406	23.8	33.5	104480	2	AC007905	AC007905 Homo sapi	C 479	23.6	33.2	179554	2	AC073268	AC073268 Homo sapi
C 407	23.8	33.5	109329	2	AL157945	AL157945 Homo sapi	C 480	23.6	33.2	182428	2	AC036167	AC036167 Homo sapi
C 408	23.8	33.5	109431	9	AC016696	AC016696 Homo sapi	C 481	23.6	33.2	182724	2	AC025279	AC025279 Homo sapi
C 409	23.8	33.5	152936	9	AC013719	AC013719 Homo sapi	C 482	23.6	33.2	183382	9	AL157388	AL157388 Human DNA
C 410	23.8	33.5	160420	2	AC097626	AC097626 Homo sapi	C 483	23.6	33.2	183920	2	AC023814	AC023814 Homo sapi
C 411	23.8	33.5	161117	2	AC008311	AC008311 Drosophill	C 484	23.6	33.2	184511	2	AC011721	AC011721 Homo sapi
C 412	23.8	33.5	164270	14	AB049735	AB049735 Gallid he	C 485	23.6	33.2	187540	2	AC073970	AC073970 Homo sapi
C 413	23.8	33.5	164270	14	AB049735	AB049735 Gallid he	C 486	23.6	33.2	188928	9	AC020612	AC020612 Homo sapi
C 414	23.8	33.5	170962	2	AL389927	AL389927 Homo sapi	C 487	23.6	33.2	189116	9	CNS01DMM	CNS01DMM Human chr
C 415	23.8	33.5	172748	2	AC097417	AC097417 Rattus no	C 488	23.6	33.2	189142	2	AC074038	AC074038 Homo sapi
C 416	23.8	33.5	173785	9	AP000355	AP000355 Homo sapi	C 489	23.6	33.2	192519	10	MM0278435	MM0278435 Mus muscu
C 417	23.8	33.5	175594	9	AL162503	AL162503 Human DNA	C 490	23.6	33.2	193101	2	AC009561	AC009561 Homo sapi
C 418	23.8	33.5	176756	2	AC099152	AC099152 Rattus no	C 491	23.6	33.2	195028	30	AC024739	AC024739 Homo sapi
C 419	23.8	33.5	177632	2	AC093615	AC093615 Homo sapi	C 492	23.6	33.2	197331	2	AC104439	AC104439 Homo sapi
C 420	23.8	33.5	177632	2	AC093615	AC093615 Homo sapi	C 493	23.6	33.2	199075	2	AC079218	AC079218 Mus muscu
C 421	23.8	33.5	180941	2	AC019219	AC019219 Homo sapi	C 494	23.6	33.2	200137	2	AC104662	AC104662 Homo sapi
C 422	23.8	33.5	182760	2	AC094052	AC094052 Rattus no	C 495	23.6	33.2	203108	2	CNS05TC3	CNS05TC3 Human chr
C 423	23.8	33.5	184476	2	AC009113	AC009113 Homo sapi	C 496	23.6	33.2	207389	9	AC090634	AC090634 Homo sapi
C 424	23.8	33.5	197225	9	AC093835	AC093835 Homo sapi	C 497	23.6	33.2	215650	2	AC090469	AC090469 Homo sapi
C 425	23.8	33.5	197360	2	AC018829	AC018829 Homo sapi	C 498	23.6	33.2	216554	2	AC095563	AC095563 Homo sapi
C 426	23.8	33.5	197748	2	AC026283	AC026283 Homo sapi	C 499	23.6	33.2	220965	2	HSJ12688	HSJ12688 Homo sapi
C 427	23.8	33.5	199938	9	AL162591	AL162591 Human DNA	C 500	23.6	33.2	223335	2	AL392187	AL392187 Homo sapi
C 428	23.8	33.5	202050	1	AL164605	AL164605 Ralstonia	C 501	23.6	33.2	223335	2	AC096334	AC096334 Rattus no
C 429	23.8	33.5	211309	2	AC011896	AC011896 Homo sapi	C 502	23.4	33.0	440	8	HS90D2R	HS90D2R Homo sapi
C 430	23.8	33.5	217442	2	AC073747	AC073747 Mus muscu	C 503	23.4	33.0	440	8	AF107133	AF107133 Picea ab
C 431	23.8	33.5	230372	2	AC073693	AC073693 Mus muscu	C 504	23.4	33.0	617	9	HSJ339116	HSJ339116 Homo sapi
C 432	23.8	33.5	236195	2	AC073713	AC073713 Mus muscu	C 505	23.4	33.0	647	9	HSJ338944	HSJ338944 Homo sapi
C 433	23.8	33.5	286550	1	SME591785	AL591785 Sinorhizo	C 506	23.4	33.0	1002	9	BC002648	BC002648 Homo sapi
C 434	23.8	33.5	303626	1	AE003601	AE003601 Drosophill	C 507	23.4	33.0	2071	3	DM032087	DM032087 Homo sapi
C 435	23.8	33.5	327773	1	AP002554	AP002554 Escherich	C 508	23.4	33.0	2071	3	DM032088	DM032088 Homo sapi
C 436	23.8	33.5	340000	1	AP001760	AP001760 Homo sapi	C 509	23.4	33.0	2071	3	DM032089	DM032089 Homo sapi
C 437	23.6	33.2	390	6	AX069537	AX069537 Sequence	C 510	23.4	33.0	2072	3	DM032090	DM032090 Homo sapi
C 438	23.6	33.2	750	9	HSJ30206	HSJ30206 Homo sapi	C 511	23.4	33.0	3009	3	AY070882	AY070882 Drosophill



512	23.4	33.0	3433	3	AY060442	Drosophill	C 585	23.2	32.7	1077	33	AC045954	AC045954 Giardia i
513	23.4	33.0	3992	3	AF033117	Drosophill	C 586	23.2	32.7	1187	1	BACESTERAS	L24749 Bacillus su
514	23.4	33.0	4119	9	AB040936	Homo sapi	C 587	23.2	32.7	1267	9	BC001809	BC001809 Homo sapi
515	23.4	33.0	4120	1	SC6D7A	Streptomy	C 588	23.2	32.7	1267	9	BC001824	BC001824 Homo sapi
516	23.4	33.0	4517	1	SC6PBNPLE	Streptomy	C 589	23.2	32.7	1267	9	BC001824	BC001824 Homo sapi
517	23.4	33.0	6290	9	HSMB01391	Streptomy	C 590	23.2	32.7	1491	9	AB018401	AB018401 Homo sapi
518	23.4	33.0	10636	1	AE005917	Caulobact	C 591	23.2	32.7	1525	1	AF056081	AF056081 Bacillus
519	23.4	33.0	10831	1	AE005917	Caulobact	C 592	23.2	32.7	1838	6	E59850	E59850 Method for
520	23.4	33.0	11011	1	AE005948	Caulobact	C 593	23.2	32.7	1954	9	AF141972	AF141972 Pongo pyg
521	23.4	33.0	14471	1	SCBAC17E8	Streptomy	C 594	23.2	32.7	2351	1	AF185273	AF185273 Burkholder
522	23.4	33.0	22775	1	SC5G8	Streptomy	C 595	23.2	32.7	2480	8	AF066635	AF066635 Chlamydom
523	23.4	33.0	31896	2	AC017879	Drosophill	C 596	23.2	32.7	3157	2	AC019519	AC019519 Drosophill
524	23.4	33.0	33154	1	AF361470	Rhizobium	C 597	23.2	32.7	3276	1	PAPBPC	PAPBPC P. aeruginos
525	23.4	33.0	39619	2	AC017644	Drosophill	C 598	23.2	32.7	3276	3	AF145637	AF145637 Streptomy
526	23.4	33.0	48975	2	AC008998	Homo sapi	C 599	23.2	32.7	3949	9	AF043897	AF043897 Homo sapi
527	23.4	33.0	50714	2	AC005471	Drosophill	C 600	23.2	32.7	4294	8	AF362957	AF362957 Aspergill
528	23.4	33.0	65088	2	AC084720	Homo sapi	C 601	23.2	32.7	4605	9	HUMPERP	D43639 Human gene
529	23.4	33.0	86824	2	AC015884	Homo sapi	C 602	23.2	32.7	4606	9	S73906	S73906 adrenomedul
530	23.4	33.0	96135	2	AC091070	Homo sapi	C 603	23.2	32.7	5400	9	AF211847	AF211847 Homo sapi
531	23.4	33.0	99395	2	AC010446	Homo sapi	C 604	23.2	32.7	6405	9	AB032946	AB032946 Homo sapi
532	23.4	33.0	108661	9	AC034214	Homo sapi	C 605	23.2	32.7	6816	6	ARI75747	ARI75747 Sequence
533	23.4	33.0	110098	9	AL358976	Human DNA	C 606	23.2	32.7	6835	6	ARI75748	ARI75748 Sequence
534	23.4	33.0	116561	9	HS753P9	Human DNA	C 607	23.2	32.7	6990	9	AF142567	AF142567 Homo sapi
535	23.4	33.0	121474	2	AC007150	Drosophill	C 608	23.2	32.7	8366	1	AF072709	AF072709 Streptomy
536	23.4	33.0	122645	2	AC058812	Homo sapi	C 609	23.2	32.7	9449	14	D84262	D84262 Hepatitis C
537	23.4	33.0	123039	2	AC093087	Homo sapi	C 610	23.2	32.7	9984	1	ASP290449	ASP290449 Amycolato
538	23.4	33.0	133155	2	AC011910	Drosophill	C 611	23.2	32.7	10126	1	AE004653	AE004653 Pseudomon
539	23.4	33.0	133765	9	HS67E13	Human DNA	C 612	23.2	32.7	11445	1	AE004490	AE004490 Pseudomon
540	23.4	33.0	143299	9	AL353619	Human DNA	C 613	23.2	32.7	12965	1	AE002048	AE002048 Deinococc
541	23.4	33.0	145068	9	HS03977B1	Human DNA	C 614	23.2	32.7	14015	1	AE0050776	AE0050776 Caulobact
542	23.4	33.0	150681	2	AC006011	Human DNA	C 615	23.2	32.7	17228	1	SC35F7	SC35F7 Streptomy
543	23.4	33.0	152118	2	AC013263	Homo sapi	C 616	23.2	32.7	18479	1	SC35F7	SC35F7 Streptomy
544	23.4	33.0	152974	2	AC0106213	Rattus no	C 617	23.2	32.7	19304	1	AB045311	AB045311 Xanthomon
545	23.4	33.0	154788	2	AC031984	Homo sapi	C 618	23.2	32.7	23764	3	AC006723	AC006723 Caenorhab
546	23.4	33.0	157134	2	AC106642	Rattus no	C 619	23.2	32.7	25595	1	AF228583	AF228583 Burkholder
547	23.4	33.0	159021	2	AC087388	Homo sapi	C 620	23.2	32.7	27854	9	AL450463	AL450463 Human DNA
548	23.4	33.0	160301	3	AC007413	Drosophill	C 621	23.2	32.7	28712	9	CNS004YVC	CNS004YVC Homo sapi
549	23.4	33.0	160457	2	AC008049	Homo sapi	C 622	23.2	32.7	29466	9	AF252549	AF252549 Homo sapi
550	23.4	33.0	163162	2	AC006247	Drosophill	C 623	23.2	32.7	29516	3	AC010840	AC010840 Drosophill
551	23.4	33.0	166009	9	AC009054	Homo sapi	C 624	23.2	32.7	36839	2	AC006181	AC006181 Homo sapi
552	23.4	33.0	170758	9	AC004965	Homo sapi	C 625	23.2	32.7	48217	9	AC073932	AC073932 Homo sapi
553	23.4	33.0	170758	9	AC004965	Homo sapi	C 626	23.2	32.7	53870	3	AE003163	AE003163 Drosophill
554	23.4	33.0	172904	3	AC007414	Drosophill	C 627	23.2	32.7	66846	2	AC105000	AC105000 Homo sapi
555	23.4	33.0	177503	9	AC005297	Homo sapi	C 628	23.2	32.7	69348	2	AC105107	AC105107 Homo sapi
556	23.4	33.0	179009	9	AC079802	Homo sapi	C 629	23.2	32.7	74436	2	AC026625	AC026625 Homo sapi
557	23.4	33.0	181321	9	AC093179	Homo sapi	C 630	23.2	32.7	77191	2	AC023381	AC023381 Homo sapi
558	23.4	33.0	182039	3	AC099026	Drosophill	C 631	23.2	32.7	77191	2	AC023381	AC023381 Homo sapi
559	23.4	33.0	187928	2	AC093624	Homo sapi	C 632	23.2	32.7	78025	2	HS780M13	HS780M13 Human DNA
560	23.4	33.0	190122	2	AC019341	Homo sapi	C 633	23.2	32.7	79726	2	AC095616	AC095616 Rattus no
561	23.4	33.0	191924	2	AC091440	Homo sapi	C 634	23.2	32.7	80680	2	AC097842	AC097842 Rattus no
562	23.4	33.0	199745	2	AL671871	Mus muscu	C 635	23.2	32.7	85378	2	AL356577	AL356577 Homo sapi
563	23.4	33.0	201050	1	AL646064	Ralstonia	C 636	23.2	32.7	96332	9	CNS07E66	CNS07E66 Human chr
564	23.4	33.0	202099	2	AC098528	Rattus no	C 637	23.2	32.7	102311	2	AC005377	AC005377 Homo sapi
565	23.4	33.0	202152	2	AC095577	Rattus no	C 638	23.2	32.7	102375	2	AC0205042	AC0205042 Homo sapi
566	23.4	33.0	206818	9	AF195953	Homo sapi	C 639	23.2	32.7	103980	9	AL354893	AL354893 Human DNA
567	23.4	33.0	209519	9	AC008397	Homo sapi	C 640	23.2	32.7	110300	2	AC020957	AC020957 Mus muscu
568	23.4	33.0	216050	1	AL646076	Ralstonia	C 641	23.2	32.7	111768	9	HS876J18	HS876J18 Human DNA
569	23.4	33.0	232156	3	AE003819	Drosophill	C 642	23.2	32.7	123530	9	AL139110	AL139110 Human DNA
570	23.4	33.0	260910	6	AE003831	Drosophill	C 643	23.2	32.7	132444	2	AL3590105	AL3590105 Homo sapi
571	23.2	32.7	141	6	AF8950	Hepatitis 4	C 644	23.2	32.7	134156	9	AL353709	AL353709 Human DNA
572	23.2	32.7	624	14	AF005102	Hepatitis	C 645	23.2	32.7	134213	9	AL357083	AL357083 Human DNA
573	23.2	32.7	639	33	AC037031	Giardia i	C 646	23.2	32.7	134570	9	CNS05TEV	CNS05TEV Human chr
574	23.2	32.7	650	9	HS4324173	Homo sapi	C 647	23.2	32.7	134570	2	AF205589	AF205589 Homo sapi
575	23.2	32.7	687	9	HS4331501	Homo sapi	C 648	23.2	32.7	138929	2	AC011868	AC011868 Homo sapi
576	23.2	32.7	785	33	AC075720	Giardia i	C 649	23.2	32.7	144015	2	AL357144	AL357144 Homo sapi
577	23.2	32.7	800	33	AC029301	Giardia i	C 650	23.2	32.7	146249	2	AL3559826	AL3559826 Homo sapi
578	23.2	32.7	829	33	AC070180	Giardia i	C 651	23.2	32.7	146547	9	HS11B24	HS11B24 Human DNA
579	23.2	32.7	855	33	AC058026	Giardia i	C 652	23.2	32.7	148181	9	AC083867	AC083867 Homo sapi
580	23.2	32.7	932	33	AC071417	Giardia i	C 653	23.2	32.7	149341	9	AC068451	AC068451 Homo sapi
581	23.2	32.7	949	33	AC041451	Giardia i	C 654	23.2	32.7	150179	9	AC034213	AC034213 Homo sapi
582	23.2	32.7	963	6	AX047849	Sequence	C 655	23.2	32.7	150393	2	AL671961	AL671961 Mus muscu
583	23.2	32.7	1009	33	AC086713	Giardia i	C 656	23.2	32.7	150583	2	AC104111	AC104111 Homo sapi
584	23.2	32.7	1014	33	AC066408	Giardia i	C 657	23.2	32.7	151097	30	AC083846	AC083846 Homo sapi

658	23.2	32.7	151272	2	AC009763	AC009763 Homo sapi	C 731	23.2	32.7	236113	2	AC023825	AC023825 Homo sapi
C 659	23.2	32.7	152422	2	AC106492	AC106492 Rattus no	C 732	23.2	32.7	239566	9	HSJ03147	AJ003147 Homo sapi
C 660	23.2	32.7	153046	2	AC095531	AC095531 Rattus no	C 733	23	32.4	502	6	AX106414	AX106414 Sequence
C 661	23.2	32.7	153825	2	AC016358	AC016358 Homo sapi	C 734	23	32.4	502	6	AX140705	AX140705 Sequence
C 662	23.2	32.7	154471	9	AC022523	AC022523 Homo sapi	C 735	23	32.4	502	6	AX200565	AX200565 Sequence
C 663	23.2	32.7	154960	2	AC011948	AC011948 Homo sapi	C 736	23	32.4	502	6	AX267221	AX267221 Sequence
C 664	23.2	32.7	155055	2	AC096379	AC096379 Rattus no	C 737	23	32.4	567	9	HSJ36826	AJ336826 Homo sapi
C 665	23.2	32.7	155263	8	AP003224	AP003224 Oryza sat	C 738	23	32.4	569	9	HSJ33684	AJ33684 Homo sapi
C 666	23.2	32.7	156066	2	AC099328	AC099328 Homo sapi	C 739	23	32.4	613	9	HSJ324177	AJ3324177 Homo sapi
C 667	23.2	32.7	156823	2	AC107948	AC107948 Homo sapi	C 740	23	32.4	650	9	HSJ32753	AJ332753 Homo sapi
C 668	23.2	32.7	157198	2	AC024082	AC024082 Homo sapi	C 741	23	32.4	651	9	HSJ337560	AJ3337560 Homo sapi
C 669	23.2	32.7	157321	9	AC068811	AC068811 Homo sapi	C 742	23	32.4	664	9	HSJ336995	AJ336995 Homo sapi
C 670	23.2	32.7	157812	2	AC055805	AC055805 Homo sapi	C 743	23	32.4	688	9	HSJ337561	AJ337561 Homo sapi
C 671	23.2	32.7	160813	2	AC108513	AC108513 Homo sapi	C 744	23	32.4	698	9	HSJ334999	AJ3334999 Homo sapi
C 672	23.2	32.7	160852	2	AC020915	AC020915 Homo sapi	C 745	23	32.4	716	9	HSJ333308	AJ3333308 Homo sapi
C 673	23.2	32.7	161459	2	AC044783	AC044783 Homo sapi	C 746	23	32.4	722	9	HSJ336807	AJ3336807 Homo sapi
C 674	23.2	32.7	162245	2	AC011008	AC011008 Homo sapi	C 747	23	32.4	756	1	PCJ132716	PCJ132716 Pseudomon
C 675	23.2	32.7	162592	2	AC074155	AC074155 Mus muscu	C 748	23	32.4	762	9	AF041430	AF041430 Homo sapi
C 676	23.2	32.7	162912	2	HSAC002067	HSAC002067 Human BAC	C 749	23	32.4	784	9	HSJ336341	AJ336341 Homo sapi
C 677	23.2	32.7	163108	2	AC016741	AC016741 Homo sapi	C 750	23	32.4	815	9	HSJ336804	AJ336804 Homo sapi
C 678	23.2	32.7	163455	10	MMU296303	MMU296303 Mus muscu	C 751	23	32.4	816	9	HSJ336874	AJ336874 Homo sapi
C 679	23.2	32.7	164008	2	AL359877	AL359877 Human DNA	C 752	23	32.4	1263	1	RCU57653	RCU57653 Rhabdobacter
C 680	23.2	32.7	164077	2	AC024398	AC024398 Homo sapi	C 753	23	32.4	1287	4	BACRYA1A	BACRYA1A Homo sapi
C 681	23.2	32.7	165159	2	AC068577	AC068577 Homo sapi	C 754	23	32.4	1347	9	BC000936	BC000936 Homo sapi
C 682	23.2	32.7	16518	2	AC007431	AC007431 Homo sapi	C 755	23	32.4	1398	9	HSJ04P501	AX078490 Sequence
C 683	23.2	32.7	166892	2	AC009969	AC009969 Homo sapi	C 756	23	32.4	2001	6	AX078490	AX078490 Sequence
C 684	23.2	32.7	168448	9	AC009469	AC009469 Homo sapi	C 757	23	32.4	2100	6	AX098220	AX098220 Sequence
C 685	23.2	32.7	168700	2	AC009115	AC009115 Homo sapi	C 758	23	32.4	3368	8	AF274672	AF274672 Vitis aesi
C 686	23.2	32.7	169089	9	AC008751	AC008751 Homo sapi	C 759	23	32.4	3773	1	PSENORC	PSENORC Pseudomonas
C 687	23.2	32.7	169284	2	AC098954	AC098954 Rattus no	C 760	23	32.4	4228	1	AF032970	AF032970 Pseudomon
C 688	23.2	32.7	169950	2	AC084049	AC084049 Homo sapi	C 761	23	32.4	5576	10	MUSMCT2A	MUSMCT2A Homo sapi
C 689	23.2	32.7	170724	2	AC021059	AC021059 Homo sapi	C 762	23	32.4	6765	10	MMU38816	MMU38816 Mus muscu
C 690	23.2	32.7	171822	2	AC011603	AC011603 Homo sapi	C 763	23	32.4	10425	1	PDENOQURE	L02534 Paracoccus
C 691	23.2	32.7	173777	2	AC098116	AC098116 Rattus no	C 764	23	32.4	10464	1	AE004634	AE004634 Pseudomon
C 692	23.2	32.7	175127	2	AC016048	AC016048 Homo sapi	C 765	23	32.4	10528	1	PCJ271325	PCJ271325 Pseudomon
C 693	23.2	32.7	175493	2	AC020769	AC020769 Homo sapi	C 766	23	32.4	10711	1	AE004489	AE004489 Pseudomon
C 694	23.2	32.7	175631	9	AC023511	AC023511 Homo sapi	C 767	23	32.4	10888	1	U32720	U32720 Haemophilus
C 695	23.2	32.7	176968	9	AC005669	AC005669 Homo sapi	C 768	23	32.4	10951	1	AE005756	AE005756 Caulobact
C 696	23.2	32.7	177241	9	HS402G11	HS402G11 Human DNA	C 769	23	32.4	11351	1	AE004510	AE004510 Pseudomon
C 697	23.2	32.7	177339	2	AC107975	AC107975 Homo sapi	C 770	23	32.4	11988	1	AE004477	AE004477 Pseudomon
C 698	23.2	32.7	177402	2	AC007406	AC007406 Homo sapi	C 771	23	32.4	12017	6	E22111	E22111 Aromatic co
C 699	23.2	32.7	179172	2	AC026331	AC026331 Homo sapi	C 772	23	32.4	12364	1	AE007167	AE007167 Mycobacte
C 700	23.2	32.7	180749	2	AC025256	AC025256 Homo sapi	C 773	23	32.4	13610	14	AE188480	AE188480 Macropodi
C 701	23.2	32.7	182441	2	AC108134	AC108134 Homo sapi	C 774	23	32.4	25381	1	SC2H2	AL450289 Streptomy
C 702	23.2	32.7	184547	2	AC074373	AC074373 Homo sapi	C 775	23	32.4	26963	1	SCC105	AL163641 Streptomy
C 703	23.2	32.7	187735	2	AC061979	AC061979 Homo sapi	C 776	23	32.4	27300	1	SCD39	AL133216 Streptomy
C 704	23.2	32.7	192381	2	AC012645	AC012645 Homo sapi	C 777	23	32.4	28951	1	HSJ161C2	Z68269 Human DNA s
C 705	23.2	32.7	193050	1	AL646062	AL646062 Rattus no	C 778	23	32.4	35292	1	MRCY36C7	MRCY36C7 Mycobacte
C 706	23.2	32.7	193101	2	AC009561	AC009561 Homo sapi	C 779	23	32.4	37186	1	MSCY244	AD000003 Mycobacte
C 707	23.2	32.7	193829	9	AC012154	AC012154 Homo sapi	C 780	23	32.4	38400	1	SC4H2	AL022268 Streptomy
C 708	23.2	32.7	194804	2	AL358253	AL358253 Homo sapi	C 781	23	32.4	39726	1	SC8D11	AL512944 Streptomy
C 709	23.2	32.7	195378	2	AL133410	AL133410 Human DNA	C 782	23	32.4	41782	1	SCG11A	AE0016952
C 710	23.2	32.7	195955	2	AC079800	AC079800 Homo sapi	C 783	23	32.4	56917	1	AME16952	Y16952 Amycolatops
C 711	23.2	32.7	196050	1	AL646058	AL646058 Rattus no	C 784	23	32.4	58707	2	AC100810	AC100810 Homo sapi
C 712	23.2	32.7	196787	2	AC104134	AC104134 Homo sapi	C 785	23	32.4	70954	2	AC104916	AC104916 Mus muscu
C 713	23.2	32.7	197445	2	AC040970	AC040970 Homo sapi	C 786	23	32.4	72383	2	AC027746	AC027746 Homo sapi
C 714	23.2	32.7	197926	2	AC010550	AC010550 Homo sapi	C 787	23	32.4	75695	2	AC025345	AC025345 Homo sapi
C 715	23.2	32.7	198402	2	AC026373	AC026373 Homo sapi	C 788	23	32.4	83373	8	ABO17064	ABO17064 Arabidops
C 716	23.2	32.7	200925	2	AC009090	AC009090 Homo sapi	C 789	23	32.4	86441	1	AL390762	AL390762 Homo sapi
C 717	23.2	32.7	202540	9	AC002524	AC002524 Homo sapi	C 790	23	32.4	86896	1	RCU57682	U57682 Rhodobacter
C 718	23.2	32.7	204058	2	AC048337	AC048337 Homo sapi	C 791	23	32.4	95808	2	AF214636	AF214636 Homo sapi
C 719	23.2	32.7	204062	2	AC026333	AC026333 Homo sapi	C 792	23	32.4	100000	2	AP000518	AP000518 Homo sapi
C 720	23.2	32.7	204653	10	AC005302	AC005302 Mus muscu	C 793	23	32.4	101369	2	AC096489	AC096489 Rattus no
C 721	23.2	32.7	205832	2	AL604066	AL604066 Mus muscu	C 794	23	32.4	104160	2	AC094039	AC094039 Rattus no
C 722	23.2	32.7	205910	2	AC044847	AC044847 Mus muscu	C 795	23	32.4	111084	9	AC006486	AC006486 Homo sapi
C 723	23.2	32.7	207050	1	AL646063	AL646063 Rattus no	C 796	23	32.4	113255	9	AP000345	AP000345 Homo sapi
C 724	23.2	32.7	207425	2	AC060790	AC060790 Homo sapi	C 797	23	32.4	114194	2	AP0093200	AP0093200 Homo sapi
C 725	23.2	32.7	210036	2	AC099782	AC099782 Homo sapi	C 798	23	32.4	117863	2	AP004550	AP004550 Homo sapi
C 726	23.2	32.7	213721	2	HS172B20	HS172B20 Human DNA	C 799	23	32.4	123436	9	AL355474	AL355474 Human DNA
C 727	23.2	32.7	218547	2	AL607024	AL607024 Mus muscu	C 800	23	32.4	123436	9	AL591435	AL591435 Human DNA
C 728	23.2	32.7	219553	10	HSJ312687	HSJ312687 Homo sapi	C 801	23	32.4	138038	2	AF004125	AF004125 Oryza sat
C 729	23.2	32.7	220119	2	AC096776	AC096776 Mus muscu	C 802	23	32.4	140108	2	AP004125	AP004125 Oryza sat
C 730	23.2	32.7	233993	2	AC110000	AC110000 Homo sapi	C 803	23	32.4	140452	10	AC006447	AC006447 Mus muscu

804	23	32.4	142776	10	AC006404	AC006404 Mus muscu	c 877	22.8	32.1	1145	1	ECU20815	U20815 Escherichia
c 805	23	32.4	146420	2	AP004621	AP004621 Oryza sat	c 878	22.8	32.1	1346	14	HS1ICP345B	M33700 Herpes simp
c 806	23	32.4	146555	2	HS1120P1.1	HS1120P1.1 Human DNA	c 879	22.8	32.1	1367	14	HS1ICP345C	M33701 Herpes simp
c 807	23	32.4	147657	2	AC016967	AC016967 Homo sapi	c 880	22.8	32.1	1399	14	HS1ICP345A	M33699 Herpes simp
c 808	23	32.4	148054	2	AC026467	AC026467 Homo sapi	c 881	22.8	32.1	1450	1	ECF1MA01	X00981 E. coli fim
c 809	23	32.4	149322	2	AC016039	AC016039 Homo sapi	c 882	22.8	32.1	1635	9	BC000681	BC000681 Homo sapi
c 810	23	32.4	151117	2	AL357128	AL357128 Homo sapi	c 883	22.8	32.1	1785	9	AK025854	AK025854 Homo sapi
c 811	23	32.4	151600	2	AP000346	AP000346 Homo sapi	c 884	22.8	32.1	1794	14	HS1ICP1	M12240 Herpes simp
c 812	23	32.4	151997	2	OSJND1010	AL607102 Oryza sat	c 885	22.8	32.1	2010	10	BC0002283	BC0002283 Mus muscu
c 813	23	32.4	153483	2	AC068899	AC068899 Mus muscu	c 886	22.8	32.1	2046	10	U00932	U00932 Mus muscu
c 814	23	32.4	153863	2	AC025361	AC025361 Homo sapi	c 887	22.8	32.1	2302	10	BC010516	BC010516 Mus muscu
c 815	23	32.4	156266	8	AP002542	AP002542 Oryza sat	c 888	22.8	32.1	2305	10	AF334736	AF334736 Mus muscu
c 816	23	32.4	157562	2	AC011574	AC011574 Homo sapi	c 889	22.8	32.1	2864	9	AF125253	AF125253 Homo sapi
c 817	23	32.4	158673	2	AC095235	AC095235 Rattus no	c 890	22.8	32.1	3143	9	BC003089	BC003089 Homo sapi
c 818	23	32.4	162248	2	AC025154	AC025154 Homo sapi	c 891	22.8	32.1	3301	9	HSMB02123	HSMB02123 Homo sapi
c 819	23	32.4	167014	2	AP004706	AP004706 Oryza sat	c 892	22.8	32.1	3395	14	OV049979	OV049979 Ory sat
c 820	23	32.4	167619	2	AL671859	AL671859 Homo sapi	c 893	22.8	32.1	3418	9	BC004181	BC004181 Homo sapi
c 821	23	32.4	167966	2	AC093398	AC093398 Bos tauru	c 894	22.8	32.1	3423	9	BC008733	BC008733 Homo sapi
c 822	23	32.4	168239	2	AC007663	AC007663 Homo sapi	c 895	22.8	32.1	3448	9	HSMB02882	HSMB02882 Homo sapi
c 823	23	32.4	169027	2	AC099282	AC099282 Rattus no	c 896	22.8	32.1	4672	9	HSFERC48	HSFERC48 Homo sapien
c 824	23	32.4	169356	2	AL671277	AL671277 Homo sapi	c 897	22.8	32.1	10765	1	AE004555	AE004555 Pseudomon
c 825	23	32.4	169599	9	AL512665	AL512665 Human DNA	c 898	22.8	32.1	10965	1	AE002004	AE002004 Deinococc
c 826	23	32.4	170408	2	AL645924	AL645924 Homo sapi	c 899	22.8	32.1	11313	1	AE000502	AE000502 Escherich
c 827	23	32.4	170650	2	AC094783	AC094783 Rattus no	c 900	22.8	32.1	14466	1	AE005662	AE005662 Escherich
c 828	23	32.4	172592	2	AC099231	AC099231 Rattus no	c 901	22.8	32.1	15335	1	AE007037	AE007037 Mycobacte
c 829	23	32.4	172613	2	AL365502	AL365502 Homo sapi	c 902	22.8	32.1	15576	1	AE007135	AE007135 Mycobacte
c 830	23	32.4	172718	2	AC096649	AC096649 Homo sapi	c 903	22.8	32.1	22947	1	MTCY4C12	MTCY4C12 Streptomy
c 831	23	32.4	174555	2	AC067739	AC067739 Homo sapi	c 904	22.8	32.1	26500	1	SC9H11	SC9H11 Mycobacteri
c 832	23	32.4	174840	2	AC006549	AC006549 Homo sapi	c 905	22.8	32.1	29120	3	AF016446	AF016446 Caenorhab
c 833	23	32.4	176463	2	AC012149	AC012149 Homo sapi	c 906	22.8	32.1	29120	3	AF016446	AF016446 Caenorhab
c 834	23	32.4	176552	2	AC024622	AC024622 Homo sapi	c 907	22.8	32.1	30000	9	HSAT27265	HSAT27265 Homo sapi
c 835	23	32.4	176628	2	AC097031	AC097031 Rattus no	c 908	22.8	32.1	30561	1	SC1F2	SC1F2 Streptomy
c 836	23	32.4	182453	2	AC091714	AC091714 Papio cyn	c 909	22.8	32.1	35716	9	AC092302	AC092302 Homo sapi
c 837	23	32.4	183976	9	AL356056	AL356056 Human DNA	c 910	22.8	32.1	36307	9	HS36BD1	HS36BD1 Human DNA s
c 838	23	32.4	184929	9	AC058790	AC058790 Homo sapi	c 911	22.8	32.1	37730	1	SC8D9	SC8D9 Streptomy
c 839	23	32.4	185167	9	AC009077	AC009077 Homo sapi	c 912	22.8	32.1	38681	1	AC004232	AC004232 Streptomy
c 840	23	32.4	185327	9	AC007224	AC007224 Homo sapi	c 913	22.8	32.1	39009	9	MTGY164	MTGY164 Mycobacteri
c 841	23	32.4	185785	2	AC084273	AC084273 Mus muscu	c 914	22.8	32.1	39150	1	SC27G11	SC27G11 Streptomy
c 842	23	32.4	186656	2	AL592143	AL592143 Homo sapi	c 915	22.8	32.1	42348	2	AC102066	AC102066 Mus muscu
c 843	23	32.4	187175	2	AC104579	AC104579 Homo sapi	c 916	22.8	32.1	49239	6	AR007269	AR007269 Sequence
c 844	23	32.4	189709	9	AL160275	AL160275 Human DNA	c 917	22.8	32.1	50341	6	AR091570	AR091570 Sequence
c 845	23	32.4	189806	9	AC021382	AC021382 Homo sapi	c 918	22.8	32.1	50341	6	AR091570	AR091570 Sequence
c 846	23	32.4	191535	2	AC022505	AC022505 Homo sapi	c 919	22.8	32.1	52297	7	ARI48205	ARI48205 Mycobacteri
c 847	23	32.4	196037	2	AL607066	AL607066 Mus muscu	c 920	22.8	32.1	52297	7	MLCGA	MLCGA Enterobacte
c 848	23	32.4	196038	2	AL161451	AL161451 Homo sapi	c 921	22.8	32.1	53425	1	EAU67194	EAU67194 Rudriivira
c 849	23	32.4	198050	1	AL646061	AL646061 Ralstonia	c 922	22.8	32.1	58996	1	AB034704	AB034704 Homo sapi
c 850	23	32.4	199414	2	AC084125	AC084125 Homo sapi	c 923	22.8	32.1	60966	9	AC003030	AC003030 Homo sapi
c 851	23	32.4	203612	2	AC098208	AC098208 Rattus no	c 924	22.8	32.1	65698	2	AC011258	AC011258 Homo sapi
c 852	23	32.4	212706	2	AC073153	AC073153 Mus muscu	c 925	22.8	32.1	67166	2	AC012546	AC012546 Homo sapi
c 853	23	32.4	213045	2	AC093640	AC093640 Homo sapi	c 926	22.8	32.1	77457	1	AF210249	AF210249 Streptomy
c 854	23	32.4	215052	2	AL590627	AL590627 Homo sapi	c 927	22.8	32.1	84077	9	AL157371	AL157371 Human DNA
c 855	23	32.4	216408	2	AC092466	AC092466 Homo sapi	c 928	22.8	32.1	87397	9	AL356778	AL356778 Human DNA
c 856	23	32.4	217992	2	AC040162	AC040162 Homo sapi	c 929	22.8	32.1	95073	2	AC007272	AC007272 Homo sapi
c 857	23	32.4	222605	9	AC010973	AC010973 Homo sapi	c 930	22.8	32.1	104131	2	AC094820	AC094820 Rattus no
c 858	23	32.4	229700	2	AC073177	AC073177 Mus muscu	c 931	22.8	32.1	108711	9	AC006037	AC006037 Homo sapi
c 859	23	32.4	236491	2	AC099290	AC099290 Rattus no	c 932	22.8	32.1	108845	1	U66917	U66917 Pseudomonas
c 860	23	32.4	349980	6	AX120085	AX120085 Sequence	c 933	22.8	32.1	110000	2	AL354714_3	AL354714_3 Continuation (4 of
c 861	23	32.4	349980	6	AX127144	AX127144 Sequence	c 934	22.8	32.1	113182	2	AC008894	AC008894 Homo sapi
c 862	22.8	32.1	294	1	PAU15326	U15326 Pseudomonas	c 935	22.8	32.1	115049	2	AC073746	AC073746 Mus muscu
c 863	22.8	32.1	344	33	AC040774	Y17093 Hyomyces d	c 936	22.8	32.1	119750	9	HSJD989D7	HSJD989D7 Human DNA
c 864	22.8	32.1	520	8	HDY17093	Y17093 Hyomyces d	c 937	22.8	32.1	120533	9	AL353717	AL353717 Human DNA
c 865	22.8	32.1	549	1	AF206650	AF206650 Escherich	c 938	22.8	32.1	123661	9	AC004518	AC004518 Homo sapi
c 866	22.8	32.1	549	1	AF206652	AF206652 Escherich	c 939	22.8	32.1	125507	9	ALA50336	ALA50336 Human DNA
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c 868	22.8	32.1	549	1	AF206658	AF206658 Escherich	c 941	22.8	32.1	128119	9	AC008101	AC008101 Homo sapi
c 869	22.8	32.1	549	1	AF206659	AF206659 Escherich	c 942	22.8	32.1	132244	2	AC093178	AC093178 Oryza sat
c 870	22.8	32.1	642	9	HSAS35297	AF206659 Escherich	c 943	22.8	32.1	137296	2	AC074162	AC074162 Mus muscu
c 871	22.8	32.1	824	14	AF251159	AF251159 Homo sapi	c 944	22.8	32.1	142839	9	AL356218	AL356218 Human DNA
c 872	22.8	32.1	832	1	HSAS29121	AF251159 Homo sapi	c 945	22.8	32.1	143250	9	AC005997	AC005997 Homo sapi
c 873	22.8	32.1	853	1	ECOPILAA	M27603 E. coli pili	c 946	22.8	32.1	144219	8	AP004194	AP004194 Oryza sat
c 874	22.8	32.1	885	6	AX079023	AX079023 Sequence	c 947	22.8	32.1	145356	9	AL513366	AL513366 Homo sapi
c 875	22.8	32.1	896	9	HSAS43354	AJ343354 Homo sapi	c 948	22.8	32.1	145456	9	AL513366	AL513366 Human DNA
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955	22.8	32.1	160655	9	AC064874	AC064874 Homo sapi
956	22.8	32.1	161798	9	AC068062	AC068062 Homo sapi
957	22.8	32.1	163444	2	AC060233	AC060233 Homo sapi
958	22.8	32.1	163924	2	AL162592	AL162592 Homo sapi
959	22.8	32.1	165799	2	AL135879	AL135879 Human DNA
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961	22.8	32.1	166118	2	OSJN00208	AL663005 Oryza sat
962	22.8	32.1	166336	9	AL445467	AL445467 Human DNA
963	22.8	32.1	166837	9	AF070718	AF070718 Homo sapi
964	22.8	32.1	168497	2	AC092410	AC092410 Bos tauru
965	22.8	32.1	168764	1	AP002569	AP002569 Escherich
966	22.8	32.1	169223	2	AL353675	AL353675 Homo sapi
967	22.8	32.1	169334	2	AC025406	AC025406 Homo sapi
968	22.8	32.1	170632	9	AL136321	AL136321 Human DNA
969	22.8	32.1	171087	9	AC073584	AC073584 Homo sapi
970	22.8	32.1	171751	2	AC094037	AC094037 Rattus no
971	22.8	32.1	172033	9	AL136131	AL136131 Human DNA
972	22.8	32.1	172862	2	AL645796	AL645796 Homo sapi
973	22.8	32.1	173039	2	CNS010VB	AL133523 Human chr
974	22.8	32.1	174666	2	AC027778	AC027778 Homo sapi
975	22.8	32.1	176268	2	AL591001	AL591001 Homo sapi
976	22.8	32.1	177344	9	AL356953	AL356953 Human DNA
977	22.8	32.1	181141	2	AC093621	AC093621 Homo sapi
978	22.8	32.1	181609	9	AC079385	AC079385 Homo sapi
979	22.8	32.1	182617	9	AC007731	AC007731 Homo sapi
980	22.8	32.1	183044	2	AC079827	AC079827 Homo sapi
981	22.8	32.1	184043	2	AC092835	AC092835 Homo sapi
982	22.8	32.1	185975	2	AC104581	AC104581 Homo sapi
983	22.8	32.1	192592	9	AC005500	AC005500 Homo sapi
984	22.8	32.1	192720	9	AC016830	AC016830 Homo sapi
985	22.8	32.1	194658	2	AC020911	AC020911 Homo sapi
986	22.8	32.1	196272	2	AC026675	AC026675 Homo sapi
987	22.8	32.1	196686	9	AC010328	AC010328 Homo sapi
988	22.8	32.1	197144	9	AC073347	AC073347 Homo sapi
989	22.8	32.1	197959	2	AP000867	AP000867 Homo sapi
990	22.8	32.1	199715	2	AC095425	AC095425 Rattus no
991	22.8	32.1	200000	2	AC006294	AC006294 Homo sapi
992	22.8	32.1	200329	10	AC078911	AC078911 Mus muscu
993	22.8	32.1	200885	2	AC012460	AC012460 Homo sapi
994	22.8	32.1	203591	1	AC007156	AC007156 Homo sapi
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996	22.8	32.1	206187	2	AC021172	AC021172 Homo sapi
997	22.8	32.1	206517	2	AP003407	AP003407 Oryza sat
998	22.8	32.1	212335	2	AL356275	AL356275 Homo sapi
999	22.8	32.1	216585	2	AP002387	AP002387 Homo sapi
1000	22.8	32.1	218634	2	AC106791	AC106791 Homo sapi

## ALIGNMENTS

RESULT 1  
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DEFINITION Homo sapiens mu opioid receptor (OPRM1) gene, partial cds, exon 1.  
ACCESSION AF024515.1 GI:2655101  
VERSION  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 305)  
Wang, J.B., Johnson, P.S., Persico, A.M., Hawkins, A.L., Griffin, C.A.  
and Uhl, G.R.  
Human mu opiate receptor. cDNA and genomic clones, pharmacologic  
characterization and chromosomal assignment

JOURNAL FEBS Lett. 338 (2), 217-222 (1994)  
MEDLINE 94139928  
REFERENCE 2 (bases 1 to 305)  
AUTHORS Bare, L.A., Mansson, E. and Yang, D.  
TITLE Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain  
JOURNAL FEBS Lett. 354 (2), 213-216 (1994)  
MEDLINE 95046336  
REFERENCE 3 (bases 1 to 305)  
AUTHORS Bergen, A.W., Kokoszka, J., Peterson, R., Long, J.C., Virkkunen, M., Linnola, M. and Goldman, D.  
TITLE Mu opioid receptor gene variants: lack of association with alcohol dependence  
JOURNAL Mol. Psychiatry 2 (6), 490-494 (1997)  
MEDLINE 98060615  
REFERENCE 4 (bases 1 to 305)  
AUTHORS Bergen, A.W., Kokoszka, J. and Goldman, D.  
TITLE Direct Submission  
JOURNAL Submitted (11-SEP-1997) Neurogenetics, NIMH/NIH, 12501 Washington Avenue, Rockville, MD 20852, USA  
COMMENT 134 US Caucasian and North American Indian chromosomes were directly sequenced at the OPRM1 locus, 5'UTR and Exon 1.  
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137  
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155  
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194  
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BASE COUNT 54 a 115 c 79 g 56 t 1 others  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.4e-10;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 153 GCAACCTGTCCGACCCATCGCGTCCGGAACCGACCGACCTGGGCGGAGAGACACACCTGT 212  
QY 61 GCCCTCCGACC 71  
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Db 213 GCCCTCCGACC 223

RESULT 2  
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LOCUS SHCC-84785 Human Homo sapiens STS genomic, sequence tagged site.  
DEFINITION G53082  
ACCESSION G53082  
VERSION G53082.1 GI:5224409  
KEYWORDS STS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 520)  
AUTHORS Olivier,M., and Cox,D.R.  
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)  
JOURNAL Unpublished

COMMENT  
Contact: Michael Olivier, David R. Cox  
Stanford Human Genome Center  
Stanford University School of Medicine  
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA  
Tel: (650) 320-5800  
Fax: (650) 320-5801  
Email: olivier@shgc.stanford.edu  
Primer A: TTTACTCTCCCTCTTTCATCCTC  
Primer B: ACTGTGCCACTTAGATGGCAAC  
STS Size: 307  
PCR Profile:  
Initial incubation: 95 degrees C for 10 minutes  
Denaturation: 94 degrees C for 30 seconds  
Annealing: 60 degrees C for 30 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9700  
Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
AmpliTaq Gold Polymerase: 0.07 units/ul  
Total Vol: 5 ul  
Buffer: MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 8.3

FEATURES  
BAC ends sequenced at TIGR from the RPC11 BAC library. Designed  
and developed at the Stanford Human Genome Center.  
Location/Qualifiers  
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STS  
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ORIGIN

Query Match 100.0%; Score 71; DB 11; Length 520;  
Best Local Similarity 100.0%; Pred. No. 2.2e-10;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACCTGCCGACCGATCGGTCCGGAACCGACCGACCTGGGCGGAGAGACACACCTGT 60  
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Db 355 GCAACCTGTCCGACCCATCGCGTCCGGAACCGACCGACCTGGGCGGAGAGACACACCTGT 296  
QY 61 GCCCTCCGACC 71  
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Db 295 GCCCTCCGACC 285

RESULT 3  
AF286024 1203 bp mRNA linear PRI 03-AUG-2000  
LOCUS Macaca mulatta mu opioid receptor mRNA, complete cds.  
DEFINITION AF286024  
ACCESSION AF286024  
VERSION AF286024.1 GI:9664878  
KEYWORDS  
SOURCE rhesus monkey.  
ORGANISM Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecoidea; Macaca.  
REFERENCE 1 (bases 1 to 1203)  
AUTHORS Miller,G.M., and Madras,B.K.  
TITLE Cloning of the Macaca mulatta mu opioid receptor  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1203)  
AUTHORS Miller,G.M., and Madras,B.K.  
TITLE Direct Submission  
JOURNAL Submitted (11-JUL-2000) Neurochemistry, New England Regional  
Primate Research Center, Harvard Medical School, One Pine Hill  
Drive, Southborough, MA 01772, USA  
Location/Qualifiers  
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/tissue\_type="striatum"  
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/protein\_id="AA97249.1"  
/db\_xref="GI:9664879"  
/translation="MDSAVPTNVSNCSTDALHSSCSPARSPGSWNI,SHLDGNLSDP  
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TATNIYIFNLALADALVSTLIPROSVYNGTWPEFTILCKIYISIDYIMFTSIFTL  
CTMSVDRIYAVCHPKALDERTPRNAKINVCNMLISSAIGLUPMFMATTKRYRGSD  
CLTFESHPSWTEMLKICVFIFALPVLITVCGTGLMLRLKSVMLSGSEKDRN  
LRRTRMVLVAVFIIICMTPIYIVIKALVLPETFTQVSWHFCIALGYNSCLN  
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EAETAPLP"

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Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACCTGCCGACCGATCGGTCCGGAACCGACCGACCTGGGCGGAGAGACACACCTGT 60  
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Db 116 GCAACCTGTCCGACCCATCGGTCCGGAACCGACCGACCTGGGCGGAGAGACACACCTGT 175  
QY 61 GCCCTCCGACC 71  
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Db 176 GCCCTCCGACC 186

RESULT 4  
AY038989 1399 bp mRNA linear PRI 15-JUL-2001  
LOCUS Macaca fascicularis mu-opioid receptor mRNA, complete cds.  
DEFINITION AY038989  
ACCESSION AY038989.1 GI:14718771  
KEYWORDS  
SOURCE crab-eating macaque.

ORGANISM Macaca fascicularis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopitheciinae; Macaca.  
REFERENCE 1 (bases 1 to 1399)  
AUTHORS Miller, G.M. and Madras, B.K.  
JOURNAL Cloning of the Macaca fascicularis mu opioid receptor  
TITLE Unpublished  
AUTHORS Miller, G.M. and Madras, B.K.  
REFERENCE 2 (bases 1 to 1399)  
TITLE Direct Submission  
AUTHORS Submitter, G.M. and Madras, B.K.  
JOURNAL Submitted (07-JUN-2001) Neurochemistry, New England Primate  
Research Center, Harvard Medical School, One Pine Hill Drive,  
Southborough, MA 01772, USA  
FEATURES  
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CTLTSPHPSWYENLTKICVEIFAEIPVLIITVCYGLMILKSVRMISGSKEDRN  
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EAETAPLP"

BASE COUNT 342 a 411 c 291 g 355 t  
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Query Match 100.0%; Score 71; DB 9; Length 1399;  
Best Local Similarity 100.0%; Pred. No. 1.9e-10;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 195 GCAACCTGTCGACCCATGCGGTCCGAACCGCAGCAGCTGGCGGAGAGAGACAGCCTGT 254  
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QY 61 GCCCTCCGACC 71  
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Db 255 GCCCTCCGACC 265  
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RESULT 5  
LOCUS ARI06017 1610 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 7 from patent US 6103492.  
ACCESSION ARI06017  
VERSION ARI06017.1 GI:12820082  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1610)  
AUTHORS Yu, L.  
TITLE Polynucleotide encoding mu opioid receptor  
JOURNAL Patent: US 6103492-A 7 15-AUG-2000.  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCCCTCCGACC 71  
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Db 414 GCCCTCCGACC 424  
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RESULT 6  
LOCUS HUMOPI01DA 1610 bp mRNA linear PRI 03-AUG-1995  
DEFINITION Homo sapiens opioid receptor mRNA, complete cds.  
ACCESSION L29301  
VERSION L29301.1 GI:459831  
KEYWORDS opioid receptor.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1610)  
AUTHORS Mestek, A., Hurley, J.H., Bye, L.S., Campbell, A.D., Chen, Y., Tian, M.,  
Liu, J., Schulman, H. and Yu, L.  
TITLE The human mu opioid receptor: modulation of functional  
desensitization by calcium/calmodulin-dependent protein kinase and  
protein kinase C  
JOURNAL J. Neurosci. 15 (3), 2396-2406 (1995)  
MEDLINE 95198115  
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CMYSDRYIAVCHPVKALDFRPNRAKIIINVCNWLSSAIGLPVFMATTKYRQSID  
CTLTSPHPSWYENLTKICVEIFAEIPVLIITVCYGLMILKSVRMISGSKEDRN  
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EAETAPLP"

BASE COUNT 384 a 467 c 359 g 400 t  
ORIGIN

Query Match 100.0%; Score 71; DB 9; Length 1610;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCCATGCGGTCCGAACCGCAGCAGCTGGCGGAGAGAGACAGCCTGT 60  
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Db 354 GCAACCTGTCGACCCATGCGGTCCGAACCGCAGCAGCTGGCGGAGAGAGACAGCCTGT 413  
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QY 61 GCCCTCCGACC 71  
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Db 414 GCCCTCCGACC 424  
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RESULT 7  
LOCUS ALI36444/c 96310 bp DNA linear PRI 06-NOV-2000  
DEFINITION Human DNA sequence from clone RP3-366F13 on chromosome 6 Contains  
ESTs, STSS, GSSs and a Cpg island. contains the OPRM1 gene encoding  
opioid receptor mu 1, complete sequence.  
ACCESSION ALI36444  
VERSION ALI36444.15 GI:9944119  
KEYWORDS HTG; Cpg island; mu 1; opioid receptor; OPRM1.

SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 96310)
REFERENCE TITLE	Kay,M. Direct Submission Submitted (06-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk requests: clonerequest@sanger.ac.uk On Aug 29, 2000 this sequence version replaced gi:9908876. During difference assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WormPEP; Information on the WormPEP database can be found at <a href="http://www.sanger.ac.uk/projects/C-elegans/wormpep">http://www.sanger.ac.uk/projects/C-elegans/wormpep</a> This sequence was generated from part of bacterial clone contigs of human Chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <a href="http://www.sanger.ac.uk/HGP/Chr6">http://www.sanger.ac.uk/HGP/Chr6</a> RP3-366F13 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <a href="http://bacpac.med.buffalo.edu/">http://bacpac.med.buffalo.edu/</a> VECTOR: pCYPAC2 IMPORTANT: This sequence is not the entire insert of clone RP3-366F13. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP3-366F13 is at 96310 in this sequence. The true right end of clone RP3-402L9 is at 100 in this sequence.
FEATURES	location/Qualifiers source 1..96310 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="6" /clone="RP3-366F13" /clone_lib="RPCI-3" 222..410 /note="MER20 repeat: matches 1..218 of consensus" repeat_region 573..722 /note="MIR repeat: matches 60..209 of consensus" 750..1020 /note="Alub repeat: matches 28..299 of consensus" 1998..2125 /note="64 copies 2 mer ta 62% conserved" 2663..2918 /note="128 copies 2 mer at 57% conserved" 2676..2825 /note="15 copies 10 mer aatatatgtt 73% conserved" 2853..2982 /note="13 copies 10 mer taatatata 63% conserved" 2982..3089 /note="54 copies 2 mer at 60% conserved" misc_feature /note="Single clone region. Assembly consistent with restriction digest." 3325..3330 /note="14 copies 4 mer atat 80% conserved" repeat_region 3276..3335 /note="6 copies 10 mer tataatatgta 78% conserved" 3392..3675
repeat_region	/note="71 copies 4 mer tcct 61% conserved" 3398..3557 /note="16 copies 10 mer ttctctctc 70% conserved" repeat_region 3399..3558 /note="80 copies 2 mer ct 69% conserved" 3565..3654 /note="9 copies 10 mer tctctcttc 76% conserved" repeat_region 3593..3678 /note="43 copies 2 mer tc 68% conserved" repeat_region 3679..3961 /note="Alub repeat: matches 3..280 of consensus" 4891..5013 /note="FLAM.C repeat: matches 1..123 of consensus" 5014..5115 /note="MIR repeat: matches 65..173 of consensus" 5346..5373 /note="14 copies 2 mer ca 96% conserved" 6416..6492 /note="MAD1 repeat: matches 3..79 of consensus" 6602..6909 /note="Alux repeat: matches 1..308 of consensus" 7645..7951 /note="Alusq repeat: matches 1..308 of consensus" 7971..8026 /note="L2 repeat: matches 2600..2660 of consensus" 8097..8567 /note="MRTH repeat: matches 40..543 of consensus" 9914..9956 /note="MAD1 repeat: matches 1..43 of consensus" complement(join(11379..12009,12783..13135,63127..63653)) mRNA /gene="OPRM1" /note="match: cDNAs: Em:S81111 Em:U00475 Em:U00442 Em:L13069 Em:L38645 Em:U35424 Em:L22455 Em:U19380 Em:U26915 Em:M96817 Em:D16829 Em:L22536 Em:L29301 Em:D16534 Em:L25119 Em:U04092 Em:E08674 Em:U02083 Em:M93273 Em:U12569 Em:AF062753 Em:L22001 Em:AF074973 Em:L11065 Em:AF074974 Em:L20684 Em:U89677 Em:D16349 Em:AF043278" /product="dl366f13.1 (opioid receptor mu 1)" /evidence-not_experimental complement(join(11379..63653) gene /gene="OPRM1" complement(join(11474..12009,12783..13135,63127..63602)) CDS /gene="OPRM1" /note="match: proteins: Sw:P33533 Sw:P33533 Sw:P32300 Sw:P41143 Tr:Q42324 Sw:P35372 Sw:P9350 Tr:O57585 Sw:P42866 Sw:Q95247 Sw:P41144 Sw:P41145 Sw:P35370" /codon_start=1 /evidence-not_experimental /product="dl366f13.1 (opioid receptor mu 1)" protein_id="CAC15482.1" /db_xref="GI:11128469" translation="MSDAQLDPLRLTLVSARTGFCKQGLMORRKEAAELGTRK VSLATSHSGARPAVSDMSAPNTASNCSTALAYSSCSPPASGVNLSHDGN LSDPGPNRTLDGGDSLCPGTSPSMITITIALYISYCAGVLGNLVIVRY TKMKATNIYIFNLALDALASTSLPSOSNYLMGMPTFCITLCXIVISIDYNNMTS IFTICTNSVDRIYAVCHVKALDRPRRNKKIINVCMLISSAIGLPWPMKATYRKQ GSIDCTLTFSHPWTWENLKIVCFITFAITMPYLITICGLHLILKSKYRLSGSKE KDRNLRTIRWLVAIVAAVIAVCIPIETFTVTQSMMHCIALGYTN SCLNIPVLAIFDENFKRCFRFCIPTSSNISNEONSTRIRONTDPHSPTANTVDNRHQ VRSLL" 13353..13654 /note="Aluo repeat: matches 3..305 of consensus" 14114..14194 /note="L2 repeat: matches 2209..2295 of consensus" 14245..14354 /note="L1MA10 repeat: matches 6206..6314 of consensus" 14326..15056 /note="match: GSS: Em:A0269347" 14355..14550 /note="MER58A repeat: matches 1..224 of consensus" 14615..15008 /note="L1ME1 repeat: matches 5633..6020 of consensus"

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repeat_region     23247..23438
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repeat_region     24601..25199
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Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      63201 GCACCTGTCGACCGATGGCTCGAACCACCGACCTGGGGGAGAGACAGCCCTGT 63242

QY      61 GCCCTCCGACC 71
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RESULT 8
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LOCUS      Homo sapiens chromosome 6 clone RP11-30607 map 6, WORKING DRAFT
DEFINITION      SEQUENCE: 18 unordered pieces.
ACCESSION      AC027439
VERSION      AC027439.2 GI:8516101
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM      Homo sapiens
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE
AUTHORS      1 (bases 1 to 182048)
              Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens chromosome 6, clone RP11-30607
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 182048)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
              Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
              Boguslavsky,L., Bouckhalter,B., Brown,A., Burkett,G.,
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              Young,G., Zainoun,J., Zimmer,A. and Zody,M.
DIRECT SUBMISSION
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 14, 2000 this sequence version replaced gi:7342168.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8135
Center clone name: 306.O.7
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 172491 bases at least Q40
Consensus quality: 177577 bases at least Q30
Consensus quality: 179465 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 180348; sum-of-contigs
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
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NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1      1047: contig of 1047 bp in length
*      1048 1147: gap of 100 bp
*      1148 1354: contig of 207 bp in length
*      1355 1454: gap of 100 bp
*      1455 3155: contig of 1701 bp in length
*      3156 3255: gap of 100 bp
*      3256 6573: contig of 3318 bp in length
*      6574 6673: gap of 100 bp
*      6674 9233: contig of 2560 bp in length
*      9234 9333: gap of 100 bp
*      9334 12513: contig of 3180 bp in length
*      12514 12613: gap of 100 bp

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* 12614 18852: contig of 6239 bp in length
* 18853 18952: gap of 100 bp
* 18953 24896: contig of 5944 bp in length
* 24897 24996: gap of 100 bp
* 24997 32904: contig of 7908 bp in length
* 32905 33004: gap of 100 bp
* 33005 41063: contig of 8059 bp in length
* 41064 41163: gap of 100 bp
* 41164 49312: contig of 8149 bp in length
* 49313 49412: gap of 100 bp
* 49413 60412: contig of 11000 bp in length
* 60413 60512: gap of 100 bp
* 60513 73244: contig of 12732 bp in length
* 73245 73344: gap of 100 bp
* 73345 88021: contig of 14677 bp in length
* 88022 88121: gap of 100 bp
* 88122 105702: contig of 17581 bp in length
* 105703 105802: gap of 100 bp
* 105803 131166: contig of 25364 bp in length
* 131167 131266: gap of 100 bp
* 131267 158770: contig of 27504 bp in length
* 158771 158870: gap of 100 bp
* 158871 182048: contig of 23178 bp in length.

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## FEATURES

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BASE COUNT 55404 a 35093 c 35419 g 54431 t 1701 others

Query Match

100.0%; Score 71; DB 2; Length 182048;

Best Local Similarity 100.0%; Pred. No. 8,5e-11;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGGTCCGAACCGACCGACCTGGCGGAGAGACACCTGT 60  
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QY 61 GCCCTCCGACC 71  
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## RESULT 9

AC021745/c

LOCUS AC021745 182383 bp DNA linear HTG 04-APR-2000

DEFINITION Homo sapiens chromosome 11 clone RP11-339D1 map 11, WORKING DRAFT

SEQUENCE 9 unordered pieces.

AC021745

AC021745.3 GI:7408033

VERSION HTG: HTGS\_PHASE1; HTGS\_DRAFT.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 182383)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 11, clone RP11-339D1

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 182383)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Beckertly,R., Beda,F.,  
Boguslavsky,L., Bouckhgalter,B., Brown,A., Burrett,G., Castle,A.,  
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,  
Dearrellano,K., Dewar,K., Domino,M., Doyle,M., Fenesator,J.,  
Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,  
Gardyna,S., Grant,G., Hagos,B., Heatford,A., Horton,L.,  
Howland,J.C., Johnson,R., Jones,C., Kann,L., Kartas,A., Klein,J.,  
Landers,T., Lehoczy,J., Levine,R., Lien,C., Liu,G., Locke,K.,  
Macdonald,P., Marquis,N., McKean,P., McGurt,A., McKernan,K.,  
McPheters,R., Meldrum,J., Menus,L., Morrow,D., Naylor,J.,  
Norman,C.H., O'Connor,T., O'Donnell,P., Ollivar,T.M., Peterson,K.,  
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,  
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,  
Stojanovic,N., Subramanian,A., Talamas,J., Testafy,S., Theodore,J.,  
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,  
Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (19-JAN-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 4, 2000 this sequence version replaced gi:6910869.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

## COMMENT

TITLE

JOURNAL

Center: Whitehead Institute/ MIT Center for Genome Research

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

Project Information

Center project name: L6050

Center clone name: 339.D.1

Summary Statistics

Sequencing vector: M13; M77815; 1008 of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 175126 bases at least Q40

Consensus quality: 178423 bases at least Q30

Consensus quality: 179878 bases at least Q20

Insert size: 184000; agarose-fp

Insert size: 181583; sum-of-contigs

Quality coverage: 4.7 in Q20 bases; agarose-fp

Quality coverage: 4.8 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 547: contig of 547 bp in length  
548 647: gap of 100 bp  
648 2304: contig of 1657 bp in length  
2305 2404: gap of 100 bp  
2405 4706: contig of 2302 bp in length  
4707 4806: gap of 100 bp  
4807 10364: contig of 5558 bp in length  
10365 10464: gap of 100 bp  
10465 22143: contig of 11679 bp in length  
22144 22243: gap of 100 bp  
22244 31783: contig of 9540 bp in length  
31784 31883: gap of 100 bp  
31884 48919: contig of 17036 bp in length  
48920 49019: gap of 100 bp  
49020 99371: contig of 50352 bp in length  
99372 99471: gap of 100 bp  
99472 182383: contig of 82912 bp in length.

FEATURES  
source  
1. 182383  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="11"  
/map="11"  
/clone="RP11-339D1"  
/clone\_11b="RPC1-11 Human Male BAC"  
1. 547  
/note="assembly-fragment  
clone\_end:Sp6  
vector\_side:left"  
648. 2304  
/note="assembly-fragment"  
2405. 4706  
/note="assembly-fragment"  
4807. 10364  
/note="assembly-fragment"  
10465. 22143  
/note="assembly-fragment"  
22244. 31783  
/note="assembly-fragment  
clone\_end:T7  
vector\_side:right"  
31884. 48919  
/note="assembly-fragment"  
49020. 99371  
/note="assembly-fragment"  
99472. 182383  
/note="assembly-fragment"

BASE COUNT 57413 a 33396 c 34191 g 56579 t 804 others  
ORIGIN

Query Match 100.0%; Score 71; DB 2; Length 182383;  
Best Local Similarity 100.0%; Pred. No. 8.5e-11;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACGTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 60  
|||||  
Db 86197 GCAACGTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 86138  
QY 61 GCCCTCGACC 71  
|||||  
Db 86137 GCCCTCGACC 86127

RESULT 10  
AX280923

LOCUS AX280923 1182 bp DNA linear PAT 02-NOV-2001  
DEFINITION Sequence 546 from Patent WO0177172.  
ACCESSION AX280923  
VERSION AX280923.1 GI:16608217  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (sites)  
REFERENCE  
AUTHORS Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.  
TITLE Non-endogenous, constitutively activated known g protein-coupled receptors  
JOURNAL Patent: WO 0177172-A 546 18-OCT-2001;  
Arena Pharmaceuticals, Inc. (US)  
FEATURES  
source  
1. 1182  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 292 a 343 c 241 g 306 t  
ORIGIN

Query Match 97.7%; Score 69.4; DB 6; Length 1182;  
Best Local Similarity 98.6%; Pred. No. 5.4e-10;  
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAACGTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 60  
|||||  
Db 116 GCAACGTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 175  
QY 61 GCCCTCGACC 71  
|||||  
Db 176 GCCCTCGACC 186

RESULT 11  
AX280921  
LOCUS AX280921 1203 bp DNA linear PAT 02-NOV-2001  
DEFINITION Sequence 544 from Patent WO0177172.  
ACCESSION AX280921  
VERSION AX280921.1 GI:16608216  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (sites)  
REFERENCE  
AUTHORS Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.  
TITLE Non-endogenous, constitutively activated known g protein-coupled receptors  
JOURNAL Patent: WO 0177172-A 544 18-OCT-2001;  
Arena Pharmaceuticals, Inc. (US)  
FEATURES  
source  
1. 1203  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 301 a 348 c 245 g 309 t  
ORIGIN

Query Match 97.7%; Score 69.4; DB 6; Length 1203;  
Best Local Similarity 98.6%; Pred. No. 5.4e-10;  
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAACGTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 60  
|||||  
Db 116 GCAACGTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 175  
QY 61 GCCCTCGACC 71  
|||||  
Db 176 GCCCTCGACC 186

RESULT 12

AR162044  
LOCUS AR162044 2160 bp DNA Linear PAT 17-OCT-2001  
DEFINITION Sequence 1 from patent US 6258556.  
ACCESSION AR162044  
VERSION AR162044.1 GI:16229099  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 2160)  
Unlabeled.  
AUTHORS Unlabeled, Johnson, P., Persico, A.M. and Wang, J. Bel.  
TITLE cDNA and genomic clones encoding human mu opiate receptor and the purified gene product  
JOURNAL Patent: US 6258556-A 1 10-JUL-2001;  
FEATURES  
location/Qualifiers  
source 1..2160  
BASE COUNT 563 a 566 c 455 g 576 t  
ORIGIN  
Query Match 97.7% Score 69.4; DB 6; Length 2160;  
Best Local Similarity 98.6%; Pred. No. 4.9e-10;  
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 GCACCTGTCGACCGACCGGTCGCGACCGACCGACCGACCGACCGCTGT 60  
DB 328 GCACCTGTCGACCGACCGGTCGCGACCGACCGACCGACCGACCGCTGT 387  
OY 61 GCCCTCCGACC 71  
DB 388 GCCCTCCGACC 398  
RESULT 13  
A87781  
LOCUS A87781 2162 bp DNA Linear PAT 22-JAN-2000  
DEFINITION Sequence 7 from Patent WO9833937.  
ACCESSION A87781  
VERSION A87781.1 GI:6736383  
KEYWORDS  
SOURCE  
ORGANISM unidentified.  
REFERENCE  
1 (bases 1 to 2162)  
unclassified.  
AUTHORS Hoehe, M. and Wendel, B.  
TITLE GENOMIC SEQUENCE OF THE HUMAN mu -OPIOID RECEPTOR GENE AND THE VARIANTS, POLYMORPHISMS AND MUTATIONS THEREOF  
JOURNAL Patent: WO 9833937-A 7 06-AUG-1998;  
HOEHE MARGRET (DE); WENDEL BIRGIT (DE)  
FEATURES  
location/Qualifiers  
source 1..2162  
BASE COUNT 562 a 565 c 458 g 575 t 2 others  
ORIGIN  
Query Match 97.7% Score 69.4; DB 6; Length 2162;  
Best Local Similarity 98.6%; Pred. No. 4.9e-10;  
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 GCACCTGTCGACCGACCGGTCGCGACCGACCGACCGACCGACCGCTGT 60  
DB 328 GCACCTGTCGACCGACCGGTCGCGACCGACCGACCGACCGACCGCTGT 387  
OY 61 GCCCTCCGACC 71  
DB 388 GCCCTCCGACC 398  
RESULT 14  
LOCUS HUMORIX  
DEFINITION Human mu opiate receptor (MOR1) mRNA, complete cds.

ACCESSION L25119  
VERSION L25119.1 GI:452072  
KEYWORDS Mu opiate receptor.  
SOURCE  
ORGANISM Homo sapiens  
REFERENCE  
Wang, J.B., Johnson, P.S., Persico, A.M., Hawkins, A.L., Griffin, C.A. and Unlabeled, G.R.  
TITLE Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterization and chromosomal assignment  
JOURNAL FEBS Lett. 338 (2), 217-222 (1994)  
MEDLINE 94139928  
FEATURES  
location/Qualifiers  
source 1..2162  
BASE COUNT 563 a 566 c 455 g 576 t 2 others  
ORIGIN  
Query Match 97.7% Score 69.4; DB 9; Length 2162;  
Best Local Similarity 98.6%; Pred. No. 4.9e-10;  
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 GCACCTGTCGACCGACCGGTCGCGACCGACCGACCGACCGACCGCTGT 60  
DB 328 GCACCTGTCGACCGACCGGTCGCGACCGACCGACCGACCGACCGCTGT 387  
OY 61 GCCCTCCGACC 71  
DB 388 GCCCTCCGACC 398  
RESULT 15  
HSU12569  
LOCUS HSU12569 1473 bp mRNA Linear PRI 12-APR-1995  
DEFINITION Human mu opioid receptor variant (MOR1) mRNA, complete cds.  
ACCESSION U12569  
VERSION U12569.1 GI:607911  
KEYWORDS  
SOURCE  
ORGANISM human.  
REFERENCE  
1 (bases 1 to 1473)  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
AUTHORS Bare, L.A., Mansson, E. and Yang, D.  
TITLE Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain  
JOURNAL FEBS Lett. 354 (2), 213-216 (1994)  
MEDLINE 95046336  
REFERENCE  
Wang, J.B., Johnson, P.S., Persico, A.M., Hawkins, A.L., Griffin, C.A. and Unlabeled, G.R.  
TITLE Human mu opiate receptor. cDNA and genomic clones, pharmacologic



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 1415)  
Simon, E.J.  
Onopriishvili, I., Andria, M.L., Viliim, F.S., Hiller, J.M. and Hiller, J.M.

JOURNAL  
MEDLINE  
99348417  
PUBMED  
10419560  
REFERENCE  
2 (bases 1 to 1344)  
Pan, Y.-X., Xu, J., Man, B.-L., Zuckerman, A.B., Rossi, G.C., Leventhal, L. and Pasternak, G.W.  
Identification and characterization of a mu-opioid receptor splice variant (MOR-1B1) unpublished

TITLE  
JOURNAL  
Submitted (29-JUN-1998) Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave, New York, NY 10021, USA

FEATURES  
source  
1. 1334  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
67..1248  
/note="alternatively spliced exon 4"  
/codon\_start=1  
/product="mu opioid receptor MOR1D"  
/protein\_id="AAB51861.1"  
/db\_xref="GI:5805153"  
/translation="MDSAGCGNISDCSDPLAPASCPAPSPSSWVNFHLEGMLSD PCKPMTLEGGSDRLCPASGSPSMITAIITIMALYSIVCVGLFENFLVMYIVRYTKM TNYIFNLADALATSTLPQSVNYLMGTWPFGLIKIVISIDYNMFTSIFT LCTMSVDRIYAVCHPVKALDERTPRNAKIVVCMWILSSAIGLPMFMATTKYRGSIDCT LTFSPHPTWYMWENLTKICVEIFAPFIMPIYIIIVCGMLIRLKSVMLSGSKERKDL RTRRMVLVYVAVPTVCMPTPIHVTITAKLITIPETTOTVSMHRCIALGYNSCLNLY LAFIDENFKRFRCFCTPIPTSTIEONSTRIRONTREHPTANTVDRTNHOLEN LEAETPLP"

CDS  
156..1361  
/note="G-protein coupled receptor"  
/codon\_start=1  
/product="mu opioid receptor"  
/protein\_id="AAB49477.2"  
/db\_xref="GI:4521326"  
/translation="MDSAGVPTNASNCTDPTHTSPSCSPAPSPSSWVNFHLEGMLSD PCKPMTLEGGSDRLCPASGSPSMITAIITIMALYSIVCVGLFENFLVMYIVRYTKM TNYIFNLADALATSTLPQSVNYLMGTWPFGLIKIVISIDYNMFTSIFT LCTMSVDRIYAVCHPVKALDERTPRNAKIVVCMWILSSAIGLPMFMATTKYRGSIDCT LTFSPHPTWYMWENLTKICVEIFAPFIMPIYIIIVCGMLIRLKSVMLSGSKERKDL RTRRMVLVYVAVPTVCMPTPIHVTITAKLITIPETTOTVSMHRCIALGYNSCLNLY LAFIDENFKRFRCFCTPIPTSTIEONSTRIRONTREHPTANTVDRTNHOLEN LEAETPLP"

BASE COUNT  
337 a 430 c 309 g 339 t

ORIGIN

Query Match  
Best Local Similarity 86.5%; Score 61.4; DB 4; Length 1415;  
Matches 65; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGCTCCGACCGACCGACCTGGCGGAGACAGACCTGT 60  
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DB 274 GCAACCTGTCGACCATCGCTCCGACCGACCGACCTGGCGGAGACAGACCTGT 333  
|||||

QY 61 GCCCTCCGACC 71  
|||||

DB 334 GCCCTCCGACC 344

RESULT 18  
AF074973 1334 bp mRNA linear ROD 31-AUG-1999  
LOCUS  
DEFINITION  
Mus musculus mu opioid receptor MOR1D mRNA, alternatively spliced, complete cds.  
AF074973  
AF074973.1 GI:5805152

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1334)  
Pan, Y.-X., Xu, J., Bolan, E., Abbadie, C., Chang, A., Zuckerman, A., Rossi, G. and Pasternak, G.W.  
Identification and characterization of three new alternatively

REFERENCE  
AUTHORS  
TITLE

spliced mu-opioid receptor isoforms  
Mol. Pharmacol. 56 (2), 396-403 (1999)

JOURNAL  
MEDLINE  
99348417  
PUBMED  
10419560  
REFERENCE  
2 (bases 1 to 1344)  
Pan, Y.-X., Xu, J., Man, B.-L., Zuckerman, A.B., Rossi, G.C., Leventhal, L. and Pasternak, G.W.  
Identification and characterization of a mu-opioid receptor splice variant (MOR-1B1) unpublished

TITLE  
JOURNAL  
Submitted (29-JUN-1998) Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave, New York, NY 10021, USA

FEATURES  
source  
1. 1334  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
67..1248  
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/codon\_start=1  
/product="mu opioid receptor MOR1D"  
/protein\_id="AAB51861.1"  
/db\_xref="GI:5805153"  
/translation="MDSAGCGNISDCSDPLAPASCPAPSPSSWVNFHLEGMLSD PCKPMTLEGGSDRLCPASGSPSMITAIITIMALYSIVCVGLFENFLVMYIVRYTKM TNYIFNLADALATSTLPQSVNYLMGTWPFGLIKIVISIDYNMFTSIFT LCTMSVDRIYAVCHPVKALDERTPRNAKIVVCMWILSSAIGLPMFMATTKYRGSIDCT LTFSPHPTWYMWENLTKICVEIFAPFIMPIYIIIVCGMLIRLKSVMLSGSKERKDL RTRRMVLVYVAVPTVCMPTPIHVTITAKLITIPETTOTVSMHRCIALGYNSCLNLY LAFIDENFKRFRCFCTPIPTSTIEONSTRIRONTREHPTANTVDRTNHOLEN LEAETPLP"

CDS  
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/note="G-protein coupled receptor"  
/codon\_start=1  
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/db\_xref="GI:4521326"  
/translation="MDSAGVPTNASNCTDPTHTSPSCSPAPSPSSWVNFHLEGMLSD PCKPMTLEGGSDRLCPASGSPSMITAIITIMALYSIVCVGLFENFLVMYIVRYTKM TNYIFNLADALATSTLPQSVNYLMGTWPFGLIKIVISIDYNMFTSIFT LCTMSVDRIYAVCHPVKALDERTPRNAKIVVCMWILSSAIGLPMFMATTKYRGSIDCT LTFSPHPTWYMWENLTKICVEIFAPFIMPIYIIIVCGMLIRLKSVMLSGSKERKDL RTRRMVLVYVAVPTVCMPTPIHVTITAKLITIPETTOTVSMHRCIALGYNSCLNLY LAFIDENFKRFRCFCTPIPTSTIEONSTRIRONTREHPTANTVDRTNHOLEN LEAETPLP"

BASE COUNT  
320 a 397 c 297 g 320 t

ORIGIN

Query Match  
Best Local Similarity 79.7%; Score 56.6; DB 10; Length 1334;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGCTCCGACCGACCGACCTGGCGGAGACAGACCTGT 60  
|||||  
DB 176 GCAACCATGTCGACCATCGCTCCGACCGACCGACCTGGCGGAGACAGACCTGT 235  
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QY 61 GCCCTCCGACC 71  
|||||

DB 236 GCCCTCCGACC 246

RESULT 19  
AF167566 1346 bp mRNA linear ROD 01-JAN-2002  
AF167566  
AF167566  
AF167566.1 GI:18026692

LOCUS  
DEFINITION  
Mus musculus mu opioid receptor variant BI mRNA, complete cds.  
AF167566  
AF167566.1 GI:18026692

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1346)  
Pan, Y.-X., Xu, J., Chang, A., Mahurter, L. and Pasternak, G.W.  
Identification and characterization of a mu-opioid receptor splice variant (MOR-1B1) unpublished

TITLE  
JOURNAL  
Submitted (12-JUL-1999) Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021, USA

REFERENCE  
AUTHORS  
TITLE

CDS

67. 1242  
/note="MOR-1B1; alternatively spliced variant of MOR-1  
gene"  
/codon\_start=1  
/product="mu opioid receptor variant B1"  
/protein\_id="AAL5582.1"  
/db\_xref="GI:18026693"

/translation="MDSAGPGNISDCSPDLAPASCSPAPGSLNLSHYDGNQSDPCG  
PNTGGSGSLCPQTPGSPSWATITMALYSIVCVGLGNEFLVYIVRYTKMTA  
TNIIYFNALADALATSTLPQSVNTLMGTWPGTICKIVISIDYNNMTSIFTLCT  
MSYDRIYAVCHPKALDFRTPRNKIVNNCNMILSSAIGLPWFMAITTKYRGSIDCT  
LTFSPHTWENLKTICVLEAFIMPVLLITVYGLMILKSRNLSGSKEDRLR  
RITRMVLVVAVFIVCGTPIHIYITIKALITIPETTFQVYSHFICALGTNSCLNPV  
LYAFIDENFKRCRFRFCIPTSSTIEQNSRIRQNTREHPSTANTVDRTNHQKIDLF"

BASE COUNT 338 a 398 c 282 g 328 t

ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 1346;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGAGCCATGCGGTCCGAAACCGACCTGGCGGGAGAGACAGCCTGT 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 176 GCAACCACTGCGAGCCATGCGGTCTTAACCGACGCGGCTTGGCGGAGACAGCCTGT 235  
QY 61 GCCCTCGACC 71  
||||| |||||  
Db 236 GCCCTGAGACC 246

RESULT 20  
AF167565 1365 bp mRNA linear ROD 01-JAN-2002  
LOCUS AF167565  
DEFINITION Mus musculus mu opioid receptor variant A mRNA, complete cds.  
ACCESSION AF167565  
VERSION AF167565.1 GI:18026690  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1365)  
Pan.Y.-X., Xu.J., Chang.A. and Pasternak.G.W.  
Identification and characterization of a mouse spliced mu-opioid  
receptor isoform (MOR-1A)  
Unpublished  
2 (bases 1 to 1365)  
Pan.Y.-X., Xu.J., Chang.A. and Pasternak.G.W.  
Direct Submission  
Submitted (12-JUL-1999) Neurology, Memorial Sloan-Kettering Cancer  
Center, 1275 York Ave., New York, NY 10021, USA  
location/Qualifiers  
1. 1365  
/organism="Mus musculus"  
/strain="CD-1"  
/db\_xref="taxon:10090"  
/chromosome="10"  
/map="10A2"  
67. 1239  
/note="MOR-1A; alternatively spliced variant of MOR-1  
gene"  
/codon\_start=1  
/product="mu opioid receptor variant A"  
/protein\_id="AAL5581.1"  
/db\_xref="GI:18026691"

/translation="MDSAGPGNISDCSPDLAPASCSPAPGSLNLSHYDGNQSDPCG  
PNTGGSGSLCPQTPGSPSWATITMALYSIVCVGLGNEFLVYIVRYTKMTA  
TNIIYFNALADALATSTLPQSVNTLMGTWPGTICKIVISIDYNNMTSIFTLCT  
MSYDRIYAVCHPKALDFRTPRNKIVNNCNMILSSAIGLPWFMAITTKYRGSIDCT  
LTFSPHTWENLKTICVLEAFIMPVLLITVYGLMILKSRNLSGSKEDRLR  
RITRMVLVVAVFIVCGTPIHIYITIKALITIPETTFQVYSHFICALGTNSCLNPV  
LYAFIDENFKRCRFRFCIPTSSTIEQNSRIRQNTREHPSTANTVDRTNHQKIDLF"

BASE COUNT 341 a 399 c 290 g 335 t

ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 1365;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGAGCCATGCGGTCCGAAACCGACCTGGCGGGAGAGACAGCCTGT 60  
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Db 176 GCAACCACTGCGAGCCATGCGGTCTTAACCGACGCGGCTTGGCGGAGACAGCCTGT 235  
QY 61 GCCCTCGACC 71  
||||| |||||  
Db 236 GCCCTGAGACC 246

RESULT 21  
RNU35424 1367 bp mRNA linear ROD 12-OCT-1995  
LOCUS RNU35424  
DEFINITION Rattus norvegicus mu opioid receptor mRNA, complete cds.  
ACCESSION U35424  
VERSION U35424.1 GI:1017731  
KEYWORDS Norway rat.  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 1367)  
Zastawny,R.L., George,S.R., Nguyen,T., Cheng,R., Tsatsos,J.,  
Briones-Urbina,R. and O'Dowd,B.F.  
Cloning, characterization, and distribution of a mu-opioid receptor  
in rat brain  
J. Neurochem. 62 (6), 2099-2105 (1994)  
MEDLINE 94246380  
REFERENCE 2 (bases 1 to 1367)  
O'Dowd,B.F.  
Direct Submission  
Submitted (05-SEP-1995) Brian F. O'Dowd, Pharmacology, University  
of Toronto, 8 Tadpole Creek Rd., Toronto, ON M5S 1A8, Canada  
location/Qualifiers  
1. 1367  
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70. 1266  
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/product="mu opioid receptor"  
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/db\_xref="GI:1017732"

/translation="MDSSTGPGNTSDCSPLAQASCSPAPGSLNLSHYDGNQSDPCG  
LNTGTGGSLSLCPQTPGSPSWATITMALYSIVCVGLGNEFLVYIVRYTKMTA  
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MSYDRIYAVCHPKALDFRTPRNKIVNNCNMILSSAIGLPWFMAITTKYRGSIDCT  
LTFSPHTWENLKTICVLEAFIMPVLLITVYGLMILKSRNLSGSKEDRLR  
RITRMVLVVAVFIVCGTPIHIYITIKALITIPETTFQVYSHFICALGTNSCLNPV  
LYAFIDENFKRCRFRFCIPTSSTIEQNSRIRQNTREHPSTANTVDRTNHQKIDLF"

BASE COUNT 325 a 421 c 306 g 315 t

ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 1367;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGAGCCATGCGGTCCGAAACCGACCTGGCGGGAGAGACAGCCTGT 60  
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Db 179 GCAACCACTGCGAGCCATGCGGTCTTAACCGACGCGGCTTGGCGGAGACAGCCTGT 238  
QY 61 GCCCTCGACC 71  
||||| |||||  
Db 239 GCCCTGAGACC 249

RESULT 22

RATMOP101D 1401 bp mRNA linear ROD 24-JAN-1994  
LOCUS Rat mu opioid receptor mRNA, complete cds.  
DEFINITION L22455  
ACCESSION L22455.1 GI:437671  
VERSION mu opioid receptor.  
KEYWORDS Rattus norvegicus (strain Sprague-Dawley) cDNA to mRNA.  
SOURCE Rattus norvegicus  
ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Rattus; Rattus norvegicus (strain Sprague-Dawley); Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 1401)  
AUTHORS Thompson, R.C., Mansour, A., Akil, H., and Watson, S.J.  
TITLE Cloning and pharmacological characterization of a rat mu opioid  
receptor  
JOURNAL Neuron 11 (5), 903-913 (1993)  
MEDLINE 94039360  
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source location/Qualifiers  
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TNIFYFNALDALATSTLPROSVNYLNGTPEFTILCKIVISIDYVMFSTIFLCT  
MSVDRTYAVCHPRKALDRTPRNAIVVNCWIISSAIGLPMEMATTKYRQGSIDCT  
LTFSPHTWYENLKIYVFIFAFIMPVLIITVCGMLRLKSVMLSGSKEDNLR  
RITRWLVVAVAFIVCWPIHIYVILKALITIPETFGTVMHFCIALGYNSCLNP  
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EAFLP"  
CDS  
BASE COUNT 330 a 434 c 312 g 325 t  
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Query Match 79.7%; Score 56.6; DB 10; Length 1401;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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QY 61 GCCCTCCGACG 71  
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DB 339 GCCCTCAGACC 349  
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REFERENCE 2 (bases 1 to 1423)  
AUTHORS Pan, Y.-X., Xu, J., Wan, B.-L., Zuckerman, A.B. and Pasternak, G.W.  
TITLE Direct Submission  
JOURNAL Submitted (04-MAY-1998) Department of Neurology, Memorial  
Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021,  
USA  
FEATURES  
source location/Qualifiers  
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LTFSPHTWYENLKIYVFIFAFIMPVLIITVCGMLRLKSVMLSGSKEDNLR  
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CDS  
BASE COUNT 343 a 423 c 317 g 340 t  
ORIGIN  
Query Match 79.7%; Score 56.6; DB 10; Length 1423;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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DB 176 GCAACGAGTCGACCATCGGTGCAACCGACGCGGCTGGCGGAGACAGCTGT 235  
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QY 61 GCCCTCCGACG 71  
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DB 236 GCCCTCAGACC 246  
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RESULT 24 AF260306 1440 bp mRNA linear ROD 22-NOV-2001  
LOCUS AF260306  
DEFINITION Mus musculus mu opioid receptor isoform MOR-1Ia mRNA, complete cds,  
alternatively spliced.  
ACCESSION AF260306  
VERSION AF260306.1 GI:17046162  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1440)  
AUTHORS Pan, Y.-X., Xu, J., Mahurter, L., Bolan, E., Xu, M. and Pasternak, G.W.  
TITLE Generation of the mu opioid receptor (MOR-1) protein by three new  
splice variants of the Opm gene  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)  
MEDLINE 11717463  
REFERENCE 2 (bases 1 to 1440)  
AUTHORS Pan, Y.-X., Xu, J., Rossi, G., Xu, M., Mahurter, L., Bolan, E. and  
Pasternak, G.W.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2000) Neurology, Memorial Sloan-Kettering Cancer  
Center, 1275 York Ave, New York, NY 10021, USA  
FEATURES  
source location/Qualifiers  
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/protein\_id="AAL34395.1"  
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/number=4  
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Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCACCTGTCCGACCCGTCGCGAAGCGACCGACCTGGCGGAGAGACAGCCTGT 60  
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Db 339 GCACCGAGTCGACCCATGCGTCTTAACCGACGCGGCGCTTGGCGGAGCAGCCTGT 398  
QY 61 GCCCTCCGACC 71  
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Db 399 GCCCTCAGACC 409  
RESULT 25  
AF400246 1440 bp mRNA linear ROD 22-NOV-2001  
LOCUS Mus musculus mu oploid receptor 1 MOR-1 mRNA, complete cds,  
DEFINITION alternatively spliced.  
ACCESSION AF400246  
VERSION AF400246.1 GI:17046392  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Pan,Y.X., Xu,J., Mahurter,L., Bolan,E., Xu,M. and Pasternak,G.W.  
TITLE Generation of the mu oploid receptor (MOR-1) protein by three new  
splice variants of the opm gene  
Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)  
JOURNAL 11717463  
PUBMED 2 (bases 1 to 1440)  
REFERENCE Pan,Y.-X., Xu,J., Rossi,G., Xu,M., Mahurter,L., Bolan,E. and  
Pasternek,G.W.  
TITLE Direct Submission  
JOURNAL Submitted (17-JUL-2001) Neurology, Memorial Sloan-Kettering Cancer  
Center, 1275 York Ave, New York, NY 10021, USA  
FEATURES  
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/db\_xref="taxon:10090"  
/chromosome="10"  
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/number=1  
99..513  
/note="alternatively spliced within exon 1"  
/number=1

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230..1426  
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MSVDRIACHPYKALDFRPRNAKIVNCGMILSSAIGLPVAFATYRROSDICT  
LTFSHPTWENLKIICVFIFAPIMVLIITVCGMLILKLSVRNLSSKEDNLR  
RITRVLVAVAFIVCMTPHIVIIKALITITPETFGVSMHFCIALGYTNSCLMPV  
LYAFIDENFRCPREFCIPTSSITIEQONSARIRONTREHPTANTVDRTNHOLENLEA  
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514..866  
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1389..>1440  
/number=4  
BASE COUNT 349 a 424 c 326 g 341 t  
ORIGIN  
Query Match 79.7%; Score 56.6; DB 10; Length 1440;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCACCTGTCCGACCCGTCGCGAAGCGACCGACCTGGCGGAGAGACAGCCTGT 60  
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Db 339 GCACCGAGTCGACCCATGCGTCTTAACCGACGCGGCGCTTGGCGGAGCAGCCTGT 398  
QY 61 GCCCTCCGACC 71  
||||| |||||  
Db 399 GCCCTCAGACC 409  
RESULT 26  
RNU02083 1448 bp mRNA linear ROD 20-JUL-1995  
LOCUS Rattus norvegicus mu oploid receptor mRNA, complete cds.  
DEFINITION Rattus norvegicus mu oploid receptor mRNA, complete cds.  
ACCESSION U02083  
VERSION U02083.1 GI:403573  
KEYWORDS  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE  
AUTHORS Bunzow,J.R., Zhang,G., Bouvier,C., Saez,C., Ronnekleiv,O.K.,  
Kelly,M.J. and Grandy,D.K.  
TITLE Characterization and distribution of a cloned rat mu-oploid  
receptor  
JOURNAL J. Neurochem. 64 (1), 14-24 (1995)  
MEDLINE 95096825  
REFERENCE 2 (bases 1 to 1448)  
AUTHORS Bunzow,J.R.  
TITLE Direct Submission  
JOURNAL Submitted (24-SEP-1993) James R. Bunzow, VIABR, Oregon Health  
Sciences University, 3181 S.W. Sam Jackson Park Rd., Portland, OR  
97201 USA  
FEATURES  
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MSVDRIYAVCHPVKALDRTPRNKATIVAVCNMISLISGLPMPFATTKYRGSDICT
LTFSHPTWENLKIYVIFAFIMPLITIVCGMLIRLKSVMGLSGSKRDNLR
RITRNLVAVAVFIVCMPTIHIYVILKALITIPETFOVSWHFCIALGYTNSCLNP
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BASE COUNT      345 a      443 c      326 g      334 t
ORIGIN
Query Match      79.7%; Score 56.6; DB 10; Length 1448;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGGTCGACCGACGACCTGGCGGAGACAGCCTGT 60
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DB 320 GCAACCACTGTCGATCGGTGTGACCGACGCGCTTGGCGGAAACGACGCTGT 379
QY 61 GCCCTCGACG 71
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DB 380 GCCCTGAGAC 390

RESULT 27      1543 bp mRNA linear ROD 31-AUG-1999
AF074974
LOCUS      Mus musculus mu opioid receptor MOR1e mRNA, alternatively spliced,
DEFINITION complete cds.
ACCESSION AF074974
VERSION AF074974.1 GI:5805154
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1543)
AUTHORS Pan,Y.X., Xu,J., Bolan,E., Abdadie,C., Chang,A., Zuckerman,A.,
Rossi,G. and Pasternak,G.W.
TITLE Identification and characterization of three new alternatively
spliced mu-opioid receptor isoforms
JOURNAL Mol. Pharmacol. 56 (2), 396-403 (1999)
MEDLINE 99348417
PUBMED 10419560
REFERENCE 2 (bases 1 to 1543)
AUTHORS Pan,Y.X., Xu,J., Man,B.-L., Zuckerman,A.B., Rossi,G.C.,
Leventhal,L. and Pasternak,G.W.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-1998) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave, New York, NY 10021, USA
FEATURES
Source Location/Qualifiers
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MSVDRIYAVCHPVKALDRTPRNKATIVAVCNMISLISGLPMPFATTKYRGSDICT
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BASE COUNT      369 a      455 c      345 g      374 t
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Query Match      79.7%; Score 56.6; DB 10; Length 1543;

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LTFSHPTWENLKIYVIFAFIMPLITIVCGMLIRLKSVMGLSGSKRDNLR
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LYAFIDENKRCRFECIPTSTSTIEQONSARLRONTREHPSANTVDRNTNQLKIDS
ORCVQHV"
BASE COUNT      369 a      455 c      345 g      374 t
ORIGIN
Query Match      79.7%; Score 56.6; DB 10; Length 1543;

Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGGTCGACCGACGACCTGGCGGAGACAGCCTGT 60
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DB 176 GCAACCACTGTCGATCGGTGTGACCGACGCGCTTGGCGGAAACGACGCTGT 235
QY 61 GCCCTCGACG 71
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DB 236 GCCCTGAGAC 246

RESULT 28      1569 bp mRNA linear ROD 22-NOV-2001
AF260308
LOCUS      Mus musculus mu opioid receptor isoform MOR-1Ja mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF260308
VERSION AF260308.1 GI:17046166
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Pan,Y.X., Xu,J., Mahutier,L., Bolan,E., Xu,M. and Pasternak,G.W.
TITLE Generation of the mu opioid receptor (MOR-1) protein by three new
splice variants of the Oprm gene
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)
PUBMED 11717463
REFERENCE 2 (bases 1 to 1569)
AUTHORS Pan,Y.X., Xu,J., Rossi,G., Xu,M., Mahutier,L., Bolan,E. and
Pasternak,G.W.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2000) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave, New York, NY 10021, USA
FEATURES
Source Location/Qualifiers
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Db 468 GCAACCACTGCGACCCATGCGGTCTTAACCGCAGGGGGCTTGGCGGAGCAGACAGCTGT 527  
QY 61 GCCCTCGGACC 71  
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Db 528 GCCCTCAGACC 538

RESULT 29  
AF400248 1569 bp mRNA linear ROD 22-NOV-2001  
LOCUS Mus musculus mu opioid receptor 1 mRNA, complete cds, alternatively  
spliced.  
ACCESSION AF400248  
VERSION AF400248.1 GI:17046396  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Pan,Y.X., Xu,J., Mahurter,L., Bolan,E., Xu,M. and Pasternak,G.W.  
TITLE 1 (bases 1 to 1569)  
JOURNAL Generation of the mu opioid receptor (MOR-1) protein by three new  
PUBMED splice variants of the opm gene  
1171/463 Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)  
REFERENCE 2 (bases 1 to 1569)  
AUTHORS Pan,Y.X., Xu,J., Rossi,G., Xu,M., Mahurter,L., Bolan,E. and  
Pasternak,G.W.  
TITLE Direct Submission  
JOURNAL Submitted (17-JUL-2001) Neurology, Memorial Sloan-Kettering Cancer  
Center, 1275 York Ave, New York, NY 10021, USA  
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Location/Qualifiers  
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/strain="CXBK"  
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<1.98  
/number=11  
exon 99..227  
/number=12  
exon 228..642  
/note="alternatively splice within exon 1"  
/number=1  
CDS 359..1555  
/note="alternatively spliced; additional translation of  
this mRNA sequence deposited in Genbank Accession Number  
AF260308"  
/codon\_start=1  
/product="mu opioid receptor 1"  
/protein\_id="AAL34509.1"  
/db\_xref="GI:17046397"  
/translation="MDSAGPGNISDCSDPLAPASGSPARGSWLNSHYDGNOSDPG  
PNRTGGGSHSLCPOTGSPSMVATITMALYSIVCVGLGNGFLVMVIVRYRMKMTA  
TNITRYFLALADALATSTLPEOSVNTIMGTWPGNLTICKIVISIDYNNMTSTFTICT  
MSVDRIACVHPKALDFRTPRNKATVNNCNMILSSAIGLPVPMATTKYRQSIDCT  
LTFSHPTWENLTKICVLFPAFIMPLIITIVCYGLMILKSVRMISGSKEDRNLR  
RTRRMVLVVAIVAVIVCMTPIHIYIIVIKALITITPETTFQVSMHFCIALGYTNSCLNP  
LVAFDENFRCFRRCFIPSTSTIEQONSARIRQNTREHSTANTVDRTHOLENLEA  
ETAPLP"

BASE COUNT 377 a 464 c 351 g 377 t  
ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 1569;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCCATGCGGTCTTAACCGCAGGGGGCTTGGCGGAGAGACAGCTGT 60

Db 468 GCAACCACTGCGACCCATGCGGTCTTAACCGCAGGGGGCTTGGCGGAGCAGACAGCTGT 527  
QY 61 GCCCTCGGACC 71  
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Db 528 GCCCTCAGACC 538

RESULT 30  
RATMORA 1586 bp mRNA linear ROD 04-AUG-1993  
LOCUS Rattus norvegicus mu opioid receptor mRNA, complete cds.  
DEFINITION Rattus norvegicus mu opioid receptor mRNA, complete cds.  
ACCESSION L13069  
VERSION L13069.1 GI:348250  
KEYWORDS mu opioid receptor.  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus Whole brain cDNA to mRNA.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
AUTHORS Chen,Y., Mestek,A., Liu,J., Hurley,J.A. and Yu,L.  
TITLE 1 (bases 1 to 1586)  
JOURNAL Molecular cloning and functional expression of a mu-opioid receptor  
MEDLINE Mol. Pharmacol. 44, 8-12 (1993)  
93341493  
FEATURES  
source 1.1586  
Location/Qualifiers  
/organism="Rattus norvegicus"  
/db\_xref="taxon:10116"  
/tissue\_type="Whole brain"  
210..1406  
/codon\_start=1  
/label=RATMOR1  
/evidence=experimental  
/product="mu opioid receptor"  
/protein\_id="AAA41650.1"  
/db\_xref="GI:348251"  
/translation="MDSSTGPGNTSDCSDPLAQAASCPARGSWLNSHYDGNOSDPG  
LNRTGGGSHSLCPOTGSPSMVATITMALYSIVCVGLGNGFLVMVIVRYRMKMTA  
TNITRYFLALADALATSTLPEOSVNTIMGTWPGNLTICKIVISIDYNNMTSTFTICT  
MSVDRIACVHPKALDFRTPRNKATVNNCNMILSSAIGLPVPMATTKYRQSIDCT  
LTFSHPTWENLTKICVLFPAFIMPLIITIVCYGLMILKSVRMISGSKEDRNLR  
RTRRMVLVVAIVAVIVCMTPIHIYIIVIKALITITPETTFQVSMHFCIALGYTNSCLNP  
LVAFDENFRCFRRCFIPSTSTIEQONSARIRQNTREHSTANTVDRTHOLENLEA  
ETAPLP"

BASE COUNT 376 a 479 c 361 g 370 t  
ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 1586;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCCATGCGGTCTTAACCGCAGGGGGCTTGGCGGAGAGACAGCTGT 60  
Db 319 GCAACCACTGCGACCCATGCGGTCTTAACCGCAGGGGGCTTGGCGGAGAGACAGCTGT 378

QY 61 GCCCTCGGACC 71  
|||||  
Db 379 GCCCTCAGACC 389

RESULT 31  
MMU26915 1610 bp mRNA linear ROD 09-NOV-1995  
LOCUS Mus musculus mu opioid receptor (MOR-1) mRNA, complete cds.  
ACCESSION U26915  
VERSION U26915.1 GI:1055230  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1610)  
AUTHORS Rossi,G.C., Pan,Y.X., Brown,G.P. and Pasternak,G.W.  
TITLE Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing and a novel morphine-6 beta-glucuronide receptor  
JOURNAL FEBS Lett. 369 (2-3), 192-196 (1995)  
MEDLINE 95377399  
REFERENCE 2 (bases 1 to 1610)  
AUTHORS Pan,Y.-X.  
TITLE Direct Submission  
JOURNAL Submitted (11-MAY-1995) Ying-Xian Pan, Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021, USA

FEATURES  
source location/Qualifiers  
1..1610  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/tissue\_type="brain"  
1..1610  
/gene="MOR-1"  
283..1479  
/gene="MOR-1"  
/codon\_start=1  
/product="mu opioid receptor"  
/protein\_id="AA81170.1"  
/db\_xref="GI:1055231"  
/translation="MDSSAGRGNISDCSDPLAPACSPAPGSLMLSHVQDNQSDPCG  
PNRTGLGSHSLCPQTGSPSMYTAITMALVSVGVLFGEFLVWYIVRTKKTA  
TNIYENLADALATSTLPQSVNVLGWTWFGNLTCKIVISIDYNNMTSIFTLCT  
MSVRYIAVCHKALDRTPEPNKIVNVCMLSSAIGLPYPMATTKYRGSDICT  
LTFSPHYWENLELKICVEIFAFIMPELVITVCGMLRLKRSVMSLGSKRKDNLR  
RTIRNVLVVAIVICMTPIPHIVYIKALITPTPTQTSVHPFALCYTKNSLNPV  
LYARIDENFKRCFRFCIPTSSTIEQNSARIRQNTREHPSTANTVDRTNHOLENLEA  
ETAPLP"

BASE COUNT 373 a 476 c 368 g 393 t  
ORIGIN

Query Match 79.7% Score 56.6; DB 10; Length 1610;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCGATCGGTCCGACCGACCGACCTGGCGGAGACAGCCTGT 60  
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Db 392 GCAACCATGTCGACCGATCGGTCTTAACCGACGCGGCGTGGCGGAGACAGCCTGT 451

QY 61 GCCCTCCGAC 71  
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Db 452 GCCCTCCGAC 462

RESULT 32  
AF260307 1614 bp mRNA linear ROD 22-NOV-2001  
LOCUS Mus musculus mu opioid receptor isoform MOR-1la mRNA, complete cds,  
DEFINITION alternatively spliced.  
ACCESSION AF260307  
VERSION AF260307.1 GI:17046164  
KEYWORDS house mouse,  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1614)  
AUTHORS Pan,Y.X., Xu,J., Mahurter,L., Bolan,E., Xu,M. and Pasternak,G.W.  
TITLE Generation of the mu opioid receptor (MOR-1) protein by three new  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)  
PUBMED 11717463  
REFERENCE 2 (bases 1 to 1614)  
AUTHORS Pan,Y.-X., Xu,J., Rossi,G., Xu,M., Mahurter,L., Bolan,E. and  
Pasternak,G.W.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2000) Neurology, Memorial Sloan-Kettering Cancer

Center, 1275 York Ave, New York, NY 10021, USA

FEATURES  
source location/Qualifiers  
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/strain="CXBK"  
/db\_xref="taxon:10090"  
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19..165  
/note="alternatively spliced; additional translation of  
this mRNA sequence deposited in Genbank Accession Number  
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/codon\_start=1  
/evidence="experimental"  
/product="mu opioid receptor isoform MOR-1la"  
/protein\_id="AAL34396.1"  
/db\_xref="GI:17046165"  
/translation="MMEAFSKSAFOKLRODGNQEGKSYLSLIPHSCLPSTORVA  
LMGC"  
99..687  
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688..1040  
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1041..1561  
/number=3  
1562..>1614  
/number=4

BASE COUNT 381 a 477 c 373 g 383 t  
ORIGIN

Query Match 79.7% Score 56.6; DB 10; Length 1614;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCGATCGGTCCGACCGACCGACCTGGCGGAGACAGCCTGT 60  
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Db 513 GCAACCATGTCGACCGATCGGTCTTAACCGACGCGGCGTGGCGGAGACAGCCTGT 572

QY 61 GCCCTCCGAC 71  
||||| |||||  
Db 573 GCCCTCCGAC 583

RESULT 33  
AF400247 1614 bp mRNA linear ROD 22-NOV-2001  
LOCUS Mus musculus mu opioid receptor 1 MOR-1 mRNA, complete cds,  
DEFINITION alternatively spliced.  
ACCESSION AF400247  
VERSION AF400247.1 GI:17046394  
KEYWORDS house mouse,  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1614)  
AUTHORS Pan,Y.X., Xu,J., Mahurter,L., Bolan,E., Xu,M. and Pasternak,G.W.  
TITLE Generation of the mu opioid receptor (MOR-1) protein by three new  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)  
PUBMED 11717463  
REFERENCE 2 (bases 1 to 1614)  
AUTHORS Pan,Y.-X., Xu,J., Rossi,G., Xu,M., Mahurter,L., Bolan,E. and  
Pasternak,G.W.  
TITLE Direct Submission  
JOURNAL Submitted (17-JUL-2001) Neurology, Memorial Sloan-Kettering Cancer  
Center, 1275 York Ave, New York, NY 10021, USA

FEATURES  
source location/Qualifiers  
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/strain="CXBK"  
/db\_xref="taxon:10090"  
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exon /number=11  
99..687  
/number=1  
404..1600  
/note="alternatively spliced; additional translation of  
this mRNA sequence deposited in GenBank Accession Number  
AF260307"  
/codon\_start=1  
/product="mu opioid receptor 1 MOR-1"  
/protein\_id="AF134508.1"  
/db\_xref="GI:17046395"  
/translation="MDSSAGPNIISDCSDPLAPASCPAPGSMILNSHVDGNSDPG  
PNRTGLGSHSLCPOTGSPSMVTATITMALYSIVCVGLNLYMYVIRYKMTA  
TNIVFINLADALATSTLPQSVNYLMWPGNICKIVISIDYNNMPTSIETCT  
MSYDRYAVCHPVALDERPNAKIVNCGMTLSSAGLPMEMATTKRROSDICT  
LFRSHPTWENLTKICVFTEAFRIIMPVITTCVGLMILKSVRLSGSKEDNR  
RITRMVLYVAIVTVCWPTPHIYIITKALITITETPTQTSMHFCIALGTNSCLNPV  
LYAFDENFRCFREFCIPTSSTIEQNSARIKONTREHPSTANTYDRTWOLENLEA  
ETAPLP"  
exon 688..1040  
/number=2  
1041..1561  
/number=3  
1562..>1614  
/number=4  
BASE COUNT 381 a 477 c 373 g 383 t  
ORIGIN  
Query Match 79.7%; Score 56.6; DB 10; Length 1614;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCAACTGTCCGACCATGCGGTCCGAACCGACCGACTGGCGGGAGAGACAGCCTGT 60  
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Db 513 GCAACAGTCCGACCATGCGGTCCGAACCGACCGACTGGCGGGAGAGACAGCCTGT 572  
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QY 61 GCCCTCGACG 71  
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Db 573 GCCCTCAGACG 583  
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RESULT 34  
LOCUS AR106013 1618 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 1 from patent US 6103492.  
ACCESSION AR106013  
VERSION AR106013.1 GI:12820078  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1618)  
AUTHORS Yu, L.  
TITLE Polynucleotide encoding mu opioid receptor  
JOURNAL Patent: US 6103492-A 1 15-AUG-2000;  
FEATURES  
source location/Qualifiers  
1..1618  
/organism="unknown"  
BASE COUNT 390 a 486 c 370 g 372 t  
ORIGIN  
Query Match 79.7%; Score 56.6; DB 6; Length 1618;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCAACTGTCCGACCATGCGGTCCGAACCGACCGACTGGCGGGAGAGACAGCCTGT 60  
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Db 323 GCAACAGTCCGACCATGCGGTCCGAACCGACCGACTGGCGGGAGAGACAGCCTGT 382  
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QY 61 GCCCTCGACG 71  
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Db 383 GCCCTCAGACG 393  
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RESULT 35  
LOCUS AR106014 1618 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 3 from patent US 6103492.  
ACCESSION AR106014  
VERSION AR106014.1 GI:12820079  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1618)  
AUTHORS Yu, L.  
TITLE Polynucleotide encoding mu opioid receptor  
JOURNAL Patent: US 6103492-A 3 15-AUG-2000;  
FEATURES  
source location/Qualifiers  
1..1618  
/organism="unknown"  
BASE COUNT 390 a 486 c 370 g 372 t  
ORIGIN  
Query Match 79.7%; Score 56.6; DB 6; Length 1618;  
Best Local Similarity 87.3%; Pred. No. 2.2e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCAACTGTCCGACCATGCGGTCCGAACCGACCGACTGGCGGGAGAGACAGCCTGT 60  
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Db 323 GCAACAGTCCGACCATGCGGTCCGAACCGACCGACTGGCGGGAGAGACAGCCTGT 582  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 61 GCCCTCGACG 71  
||||| |||||  
Db 383 GCCCTCAGACG 393  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
RESULT 37  
LOCUS AR153355 1618 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 3 from patent US 6235496.  
ACCESSION AR153355  
VERSION AR153355.1 GI:15120887  
QY 1 GCAACTGTCCGACCATGCGGTCCGAACCGACCGACTGGCGGGAGAGACAGCCTGT 60  
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Db 323 GCAACAGTCCGACCATGCGGTCCGAACCGACCGACTGGCGGGAGAGACAGCCTGT 382  
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QY 61 GCCCTCGACG 71  
||||| |||||  
Db 383 GCCCTCAGACG 393  
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KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1618)  
AUTHORS Yu, L.  
TITLE Nucleic acid encoding mammalian mu opiod receptor  
JOURNAL Patent: US 6235496-A 3 22-MAY-2001;  
FEATURES Location/Qualifiers  
source 1..1618  
/organism="unknown"  
BASE COUNT 390 a 486 c 370 g 372 t  
ORIGIN  
Query Match 79.7%: Score 56.6; DB 6; Length 1618;  
Best Local Similarity 87.3%: Pred. No. 2.2e-06;  
Matches 62: Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCAACCTGTCGACCATCGGTCCGACCGCAGCCTGTGGCGGAGAGACAGCCTGT 60  
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Db 323 GCAACCACTCCGATCCGATCGGTCTGAACCGCAGCGGCTTGGCGGAGACAGCCTGT 382  
QY 61 GCCCTCCGACC 71  
||||| |||||  
Db 383 GCCCTCAGACC 393  
RESULT 38  
AF167568 1729 bp mRNA linear ROD 28-JUN-2000  
LOCUS AF167568  
DEFINITION Mus musculus mu opiod receptor variant F mRNA, complete cds.  
ACCESSION AF167568  
VERSION AF167568.1 GI:8778197  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1729)  
AUTHORS Pan, Y.-X., Xu, J., Bolan, E., Chang, A., Mahurter, L., Rossi, G. and  
Pasternak, G.W.  
TITLE Isolation and expression of a novel alternatively spliced mu opiod  
JOURNAL receptor isoform, MOR-1F  
MEDLINE FEBS Lett. 466 (2-3), 337-340 (2000)  
20145060  
PUBMED 10682855  
REFERENCE 2 (bases 1 to 1729)  
AUTHORS Pan, Y.-X., Xu, J., Chang, A., Mahurter, L. and Pasternak, G.W.  
TITLE Direct Submission  
JOURNAL Submitted (13-JUN-2000) Neurology, Memorial Sloan-Kettering Cancer  
Center, 1275 York Ave., New York, NY 10021, USA  
FEATURES Location/Qualifiers  
source 1..1729  
/organism="Mus musculus"  
/strain="CD-1"  
/db\_xref="taxon:10090"  
/chromosome="10"  
/map="10A2"  
67..1401  
/note="MOR-1F: alternatively spliced variant of MOR-1  
gene"  
/codon\_start=1  
/product="mu opiod receptor variant F"  
/protein\_id="AA79213.1"  
/db\_xref="GI:8778198"  
/translation="MDSSAGPNTSDCDPLAPASCPAPGSWLNSHVDGNOSDPCG  
PNTGLGSHSLCPQSGSPMVAITITMALYSICVYGLFGNFIWMYIVRYTKMTA  
TNIYENLALADALATSLPPOSVNYMTGMPENCIKIVISIDYNNMFTSLTCT  
MSVDRYIAGCHPVKALDEPRNKAIVNVCNMILSSAIGPVNMTATYKROGSDCT  
LITSHPTWYENLTKICVFIFATIMPVLTITVCGMLILRLKSVRLSGSKEDRNLR  
RTRMVLVVAIVAVELICWTFPIHIVITIALITITPTTQTVSMHCIALGYSNCLNF  
LYAFIDNFKRCFREFCIPISSTLEONSARIRONTREHPSTANTVDRTHQACACV  
PGANRGOTKASDLIDLELFTVSGHQADAEINPGPYEGSKCAEPLAISLVPY"

BASE COUNT 417 a 505 c 395 g 412 t  
ORIGIN  
Query Match 79.7%: Score 56.6; DB 10; Length 1729;  
Best Local Similarity 87.3%: Pred. No. 2.2e-06;  
Matches 62: Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCAACCTGTCGACCATCGGTCCGACCGCAGCCTGTGGCGGAGAGACAGCCTGT 60  
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Db 176 GCAACCACTCCGATCCGATCGGTCTTAACCGCAGCGGCTTGGCGGAGACAGCCTGT 235  
QY 61 GCCCTCCGACC 71  
||||| |||||  
Db 236 GCCCTCAGACC 246  
RESULT 39  
AF167567 1944 bp DNA linear ROD 17-FEB-1996  
LOCUS AF167567  
DEFINITION mu opiod receptor (exon 1, promoter) [rats, Genomic, 1944 nt].  
ACCESSION AF167567  
VERSION AF167567.1 GI:1195532  
KEYWORDS  
SOURCE Rattus sp.  
ORGANISM Rattus sp.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 1944)  
AUTHORS Kraus, J., Horn, G., Zimprich, A., Simon, T., Mayer, P. and Hollt, V.  
TITLE Molecular cloning and functional analysis of the rat mu opiod  
JOURNAL receptor gene promoter  
MEDLINE Biochem. Biophys. Res. Commun. 215 (2), 591-597 (1995)  
96011819  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gidsbg 172339] from the original journal article.  
This sequence comes from Fig. 1.  
FEATURES Location/Qualifiers  
source 1..1944  
/organism="Rattus sp."  
/db\_xref="taxon:10118"  
1361..>1944  
1661..1944  
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gene  
mRNA  
gene  
BASE COUNT 498 a 468 c 446 g 532 t  
ORIGIN  
Query Match 79.7%: Score 56.6; DB 10; Length 1944;  
Best Local Similarity 87.3%: Pred. No. 2.1e-06;  
Matches 62: Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCAACCTGTCGACCATCGGTCCGACCGCAGCCTGTGGCGGAGAGACAGCCTGT 60  
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Db 1770 GCAACCACTCCGATCCGATCGGTCTGAACCGCAGCGGCTTGGCGGAGACAGCCTGT 1829  
QY 61 GCCCTCCGACC 71  
||||| |||||  
Db 1830 GCCCTCAGACC 1840  
RESULT 40  
AF167567 2045 bp mRNA linear ROD 01-JAN-2002  
LOCUS AF167567  
DEFINITION Mus musculus mu opiod receptor variant B11 mRNA, complete cds.  
ACCESSION AF167567  
VERSION AF167567.1 GI:18026694  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2045)

AUTHORS Pan, Y.-X., Xu, J., Chang, A., Mahurter, L. and Pasternak, G.W.  
TITLE Identification and characterization of a novel mu opioid receptor splice variant (MOR-1BII)  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2045)  
AUTHORS Pan, Y.-X., Xu, J., Chang, A. and Pasternak, G.W.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUL-1999) Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021, USA  
FEATURES  
source  
1. 2045  
/organism="Mus musculus"  
/strain="CD-1"  
/db\_xref="taxon:10090"  
/chromosome="10"  
/map="10A2"  
67..1296  
/note="MOR-1BII: alternatively spliced variant of MOR-1 gene"  
/codon\_start=1  
/product="mu opioid receptor variant BII"  
/protein\_id="AA15583.1"  
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/translation="MDSNAGPNTISDCSPPLAPASCPAPGSLNLSHYDGNQSDPCGPNRTGLGSHSLCPOTGSPSWATITIMALYSIVCVGLFNGFLVMYIVRTKMTATNIIYFNLALADALATSTLPQSVNTLMGTGPNGLIVISIDYNNMTSIFLTCTMSVDRIYAVCHADPVALDFTPTPRNAKIVNQCMTLSSAIGLIPVFNATITTYRQGSIDCTLFSHPITWVENLTKICVFIAPFIMPVLTIVCYGMILKSVRLSGSKEDRNLRITRWLVVAVVAVIVCMTPIHIVIIKILITIDETFORVSMHFCALGTNSCLNPLVLYAFIDENKRCRCRECIPTSSITIEQONARIRONIREHPSTANTYDRINHOXLMWRAMPFRRLHIALMSLDN"  
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Best local Similarity 87.3%; Pred. No. 2,1e-06;  
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QY 1 GCAACCTGTCCGACCCATGGGTCCGACCGACCTGGGGGAGAGACAGCCTGT 60  
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Db 176 GCAACCAAGTCCGACCGATGGGTCTTAACCGACGGGGCTTGGGGAGGACAGCCTGT 235  
QY 61 GCCCTCGACG 71  
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Db 236 GCCCTCAGAC 246  
RESULT 41  
MMOR1 2093 bp DNA linear ROD 08-NOV-1994  
LOCUS Mus musculus mu opioid receptor (MOR) gene, exon 1.  
ACCESSION U10558  
VERSION U10558.1 GI:565065  
KEYWORDS 1 of 4  
SEGMENT house mouse.  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 2084)  
AUTHORS Min, B.H., Augustin, L.B., Felsheim, R.F., Fuchs, J.A. and Loh, H.H.  
TITLE Genomic structure analysis of promoter sequence of a mouse mu opioid receptor gene  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (19), 9081-9085 (1994)  
MEDLINE 94377496  
REFERENCE 2 (bases 1 to 2093)  
AUTHORS Augustin, L.B.  
TITLE Direct Submission  
JOURNAL Submitted (13-JUN-1994) Lance B. Augustin, Pharmacology, University of Minnesota, 435 Delaware Street SE, Minneapolis, MN 55455, USA  
FEATURES  
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intron 2085..>2093  
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Db 1910 GCAACCAAGTCCGACCGATGGGTCTTAACCGACGGGGCTTGGGGAGGACAGCCTGT 1969  
QY 61 GCCCTCGACG 71  
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Db 1970 GCCCTCAGAC 1980  
RESULT 42  
AR148257 2135 bp DNA linear PAT 08-AUG-2001  
LOCUS AR148257  
DEFINITION Sequence 1 from patent US 6225080.  
ACCESSION AR148257  
VERSION AR148257.1 GI:15112347  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2135)  
AUTHORS Uhl, G.R., Eppler, C.Mark. and Wang, J.-B.  
TITLE Mu-subtype opioid receptor  
JOURNAL Patent: US 6225080-A 1 01-MAY-2001;  
FEATURES  
source  
1. 2135  
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Best local Similarity 87.3%; Pred. No. 2,1e-06;  
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QY 61 GCCCTCGACG 71  
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Db 200 GCCCTCAGAC 210  
RESULT 43  
RATMOR1A 2135 bp mRNA linear ROD 21-OCT-1993  
LOCUS RATMOR1A  
DEFINITION Rattus norvegicus Mu opiate receptor (MOR1) mRNA, complete cds.  
ACCESSION L20684  
VERSION L20684.1 GI:409149  
KEYWORDS Mu opiate receptor.  
SOURCE Rattus norvegicus (library: lambda ZAP (Stratagene)) cortex cDNA to

ORGANISM mRNA.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 2135)  
AUTHORS Wang, J.-B., Imai, Y., Epier, M.C., Gregor, P., Spiwak, C. and Uhl, G.R.  
TITLE Mu opiate receptor: cDNA cloning and expression  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 10230-10234 (1993)  
MEDLINE 94052137  
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31..1227  
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MSVDRIYAVCHPVKALDRTPRNAKIYVNCMISSAIGLPVMEATTKYRQGSIDCT  
LTFSPHYWENLTKICVFIFAFIMPVLITITVCGGLMLRLKSYMLSGSKERDNL  
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BASE COUNT 541 a 590 c 441 g 563 t

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Query Match 79.7%; Score 56.6; DB 10; Length 2135;  
Best Local Similarity 87.3%; Pred. No. 2.1e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 GCACCTGTCGACCATCGCTCGACGACGACGACTGGCGGAGACAGACCTGT 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 140 GCACCATGTCGACCATCGCTCGACGACGACGACTGGCGGAGACAGACCTGT 199

OY 61 GCCCTCGACG 71  
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Db 200 GCCCTCGACG 210

RESULT 44  
AB047546 2137 bp mRNA linear ROD 22-AUG-2001  
LOCUS AB047546  
DEFINITION Mus musculus MOR mRNA for mu opioid receptor, complete cds.  
ACCESSION AB047546.1 GI:15277133  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2137)  
AUTHORS Ikeda, K., Kobayashi, T., Ichikawa, T., Kumanishi, T., Niki, H. and  
Yano, R.  
TITLE The untranslated region of m-opioid-receptor mRNA contributes to  
reduced opioid sensitivity in CXBR mice  
J. Neurosci. (2000) In press  
2 (bases 1 to 2137)  
AUTHORS Ikeda, K.  
TITLE Direct Submission  
JOURNAL Submitted (21-AUG-2000) Kazutaka Ikeda, RIKEN Brain Science  
Institute, Neurobiology of Emotion Laboratory; 2-1 Hirotsawa, Wako,  
Saitama 351-0198, Japan (E-mail: Ikeda.k@postnu.riken.go.jp,  
Tel: 81-48-462-1111 (ex. 6436), Fax: 81-48-467-9645)  
FEATURES  
Location/Qualifiers

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LTFSPHYWENLTKICVFIFAFIMPVLITITVCGGLMLRLKSYMLSGSKERDNL  
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ETAPLP"

BASE COUNT 540 a 581 c 471 g 545 t

ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 2137;  
Best Local Similarity 87.3%; Pred. No. 2.1e-06;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 GCACCTGTCGACCATCGCTCGACGACGACGACTGGCGGAGACAGACCTGT 60  
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Db 324 GCACCATGTCGACCATCGCTCGACGACGACGACTGGCGGAGACAGACCTGT 383

OY 61 GCCCTCGACG 71  
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Db 384 GCCCTCGACG 394

RESULT 45  
A68824 2229 bp DNA linear PAT 06-MAY-1999  
LOCUS A68824  
DEFINITION Sequence 1 from Patent WO9802534.  
ACCESSION A68824  
VERSION A68824.1 GI:4759752  
KEYWORDS  
SOURCE  
ORGANISM  
unidentified.  
unclassified.  
1 (bases 1 to 2229)  
REFERENCE Kieffer, B.L., Matthies, H.W., Simonin, F.H., Dietrich, A. and Lemaire, M.  
AUTHORS TRANSGENIC ANIMAL WHOSE EXPRESSION OF THE OPIATE RECEPTORS IS  
TITLE MODIFIED  
JOURNAL Patent: WO 9802534-A 1 22-JAN-1998;  
CENTRE NAT RECH SCIENT (FR)  
COMMENT Other publication FR 2750825 19980116.  
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source location/Qualifiers  
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/db\_xref="taxon:32644"  
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LYAFIDENFKRCFREFCIPSTSTIEQNSARIQNTREHPSTANTVDRTNHLENLEA  
ETAPLP"

BASE COUNT 562 a 608 c 489 g 570 t





Db	293	GCAACCACTCCGATCCATCGGGTGTCTGAACCGAGCACC GGCGCTTTGGCGGGAACCAACCAACCCCTGT	352
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Db	353	GCCCTCACACC 363	
RESULT 48			
LOCUS	AC055776		
DEFINITION	Mus musculus chromosome 10 clone RP23-11015 map 10,	linear	HTG 04-MAY-2001
ACCESSION	AC055776	178454 bp	DNA
VERSION	AC055776.2	GI:9369492	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 178454)		
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.		
TITLE	Mus musculus chromosome 10, clone RP23-11015		
JOURNAL	Unpublished		
REFERENCES	2 (bases 1 to 178454) Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beka,F., Boguslavsky,I., Boukhgalter,B., Brown,A., Burkett,G., Campioiano,A., Castle,A., Choquel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodghe,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glind,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heathford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGraw,P., McKenna,K., McPheters,R., Melidiniy,M., Menusz,L., Minova,T., Miranda,C., Mlegwa,P., Morrow, Murphy,T., Naylor,T., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanti,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tsaijaye,S., Theodore,J., Tittrell,A., Travers,M., Trigilio,J., Vassilay,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and zody,M.		
TITLE	Submitted (18-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
JOURNAL	On Jul22, 2000 this sequence version replaced gi:17582600.		
COMMENT			

CAACCAGTCGCATCATCGGGCTCTGACCGCAGCGGGCTTGCGGGGACGACAGCCTCT 352

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 11111 1111  
 CCGCTCAGACC 363

AC055776 178454 bp DNA linear HTG 04-MAY-2001  
 Mus musculus chromosome 10 clone RP23-11015 map 10, WORKING DRAFT  
 SEQUENCE, 21 unordered pieces.  
 AC055776  
 AC055776.2 GI:9369492  
 HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
 Mus musculus  
 house mouse.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 178454)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 Mus musculus chromosome 10, clone RP23-11015  
 Unpublished  
 2 (bases 1 to 178454)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Balow,J., Barna,N., Bastien,V., Beda,F.,  
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 Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,  
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,  
 Galagan,J., Gardyna,S., Ginde,S., Goyette,W., Graham,L.,  
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
 Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,  
 Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Marquis,N.,  
 McCarthy,M., McEwan,P., McGuck,A., McKernan,K., McPheters,R.,  
 Melgrim,J., Menes,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,  
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Olivar,T.M., Oliver,J.D., Peterson,K., Pierre,N.,  
 Pisanici,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
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 Testa,S., Theodore,J., Tittell,A., Travers,M., Trigilio,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (18-APR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jul 22, 2000 this sequence version replaced g1:7582600.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www.seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu

Project Information

Center project name: L5746

Center clone name: 11.015

Summary Statistics

Sequencing vector: M13; M77815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 16586 bases at least Q40  
 Consensus quality: 172885 bases at least Q30  
 Consensus quality: 175270 bases at least Q20  
 Insert size: 190000; agarose-1p  
 Insert size: 176454; sum-of-ctrls  
 Quality coverage: 4.5 in Q20 bases; agarose-1p  
 Quality coverage: 4.8 in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently

* consists of 21 contigs. The true order of the pieces	
* is not known and their order in this sequence record is	
* arbitrary. Gaps between the contigs are represented as	
* runs of N, but the exact sizes of the gaps are unknown.	
* This record will be updated with the finished sequence	
* as soon as it is available and the accession number will	
* be preserved.	
* 1	1545: contig of 1545 bp in length
* 100 bp	
* 1546 1645: gap of	100 bp
* 1646 2950: contig of 1305 bp in length	
* 2951 3050: gap of	100 bp
* 3051 5112: contig of 2062 bp in length	
* 5113 5212: gap of	100 bp
* 5213 8232: contig of 3020 bp in length	
* 8233 8332: gap of	100 bp
* 8333 13079: contig of 4747 bp in length	
* 13080 13179: gap of	100 bp
* 13180 16940: contig of 3761 bp in length	
* 16941 17040: gap of	100 bp
* 17041 21192: contig of 4152 bp in length	
* 21193 21292: gap of	100 bp
* 21293 26578: contig of 5286 bp in length	
* 26579 26678: gap of	100 bp
* 26679 32608: contig of 5930 bp in length	
* 32609 32708: gap of	100 bp
* 32709 38888: contig of 6180 bp in length	
* 38889 38988: gap of	100 bp
* 38989 44556: contig of 5566 bp in length	
* 44557 44656: gap of	100 bp
* 44657 51768: contig of 7112 bp in length	
* 51769 51868: gap of	100 bp
* 51869 58681: contig of 6813 bp in length	
* 58682 58781: gap of	100 bp
* 58782 65622: contig of 6841 bp in length	
* 65623 65722: gap of	100 bp
* 65723 77537: contig of 11815 bp in length	
* 77538 77637: gap of	100 bp
* 77638 85102: contig of 7465 bp in length	
* 85103 85202: gap of	100 bp
* 85203 99219: contig of 14017 bp in length	
* 99220 99319: gap of	100 bp
* 99320 110889: contig of 11570 bp in length	
* 110890 110989: gap of	100 bp
* 110990 132713: contig of 21724 bp in length	
* 132714 132813: gap of	100 bp
* 132814 152788: contig of 19975 bp in length	
* 152789 152888: gap of	100 bp
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26679. 32608	

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ACCESSION	Sequence AX346295	1366 from Patent WO020928.			
VERSION	AX346295.1	GI:18494181			
KEYWORDS	.				
SOURCE	synthetic construct.				
ORGANISM	synthetic construct				
REFERENCE	artificial sequence.				
AUTHORS	1 (sites)				
TITLE	Olek,A., Piepenbrock,C. and Berlin,K.				
JOURNAL	Diagnosis of diseases associated with the immune system				
	Patent: WO 0200928-A 1366 03-JAN-2002;				
	Epigenomics AG (DE)				
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	/db_xref="taxon:32630"				
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ORIGIN					

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Best Local Similarity	81.4%	Pred No. 0.00022		
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D8	1174	CAACCTATCCGAGCCCATACGATCCGAACCGCACCAGCACTAAACGAAAAAACCAACTATA	1115					
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D8	1114	CCCTCCGACC	1105					

RESULT	50		
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LOCUS	AX348524	6494 bp	DNA
DEFINITION	Sequence 32 from Patent WO0202809.		linear
			PAT 06-FEB-2002

VERSION AX348524.1 GI:18614559

SOURCE synthetic construct.

artificial sequence.

**AUTHORS**  
Olek, A., Piepenbrock, C. and Berlin, K

cancer  
NO 0000000 , 22 10 JAN 2003

Epigenomics AG (DE)

source 1. .6494

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/db_xref="taxon:32630"

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/Note="chemically treated genomic DNA (Homo sapiens)"
BASE COUNT      1929 a      81 c    1179 g    3305 t
ORIGIN

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Query Match	69.3%	Score	49.2	DB	6	Length	6494
Best Local Similarity	81.4%	Pred. NO.	0.00022				
Matches	57	Conservative	0	Mismatches	13	Indels	0
						Gaps	0

Qy 2 CAACCTGTCCGACCATTGCCTGCCAACCAGCAGCTGGCGGGAGAGAACACGCTGTG 61  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1174 CAACCTATCCGACCATTACGATCCGAACCGCACCACTTAACGAAAAACAACCTATA 115

QY	62	CCCTCCGACC	71
Db	1114	CCCTCCGACC	1105

Search completed: November 1, 2002, 17:03:11  
Job time : 2172 secs

Search completed: November 1, 2002, 17:03:11  
Job time : 2172 secs

Search completed: November 1, 2002, 17:03:11  
Job time : 2172 secs



83	23.8	33.5	776	22	AAK53404	Human polynucleoti	c 156	22.8	32.1	597	20	AAK77454	E. coli strain HBI
c 84	23.8	33.5	2181	20	AAK07446	Rhodothermus marin	157	22.8	32.1	885	22	AAK26439	Pseudomonas sp hea
c 85	23.8	33.5	2181	21	AAZ89961	Isozymylase nucleot	158	22.8	32.1	1281	13	AAQ23296	HSV-1 (MGH-10) ICP
c 86	23.8	33.5	2376	20	AAK16153	Mouse Sox1 cDNA.	159	22.8	32.1	1303	13	AAQ23297	HSV-1 (CVO-2) ICP3
c 87	23.8	33.5	2802	20	AAK52420	Human polynucleoti	160	22.8	32.1	1335	13	AAQ23295	HSV-1 (F) ICP34.5
c 88	23.8	33.5	3024	23	ABLI17103	Drosophila melanog	c 161	22.8	32.1	2208	21	AAK21847	Human breast and o
c 89	23.8	33.5	5654	23	ABLI17102	Drosophila melanog	c 162	22.8	32.1	10820	22	ABAI16598	Human nervous syst
c 90	23.8	33.5	24553	22	AAK27689	DNA encoding novel	c 163	22.8	32.1	50341	19	AAK26574	DNA sequence of a
c 91	23.6	33.2	390	22	AAK64253	Novel human polynu	c 164	22.8	32.1	50341	21	AAK39519	L5 shuttle phasid
c 92	23.6	33.2	415	21	AAK30086	Human colon cancer	c 165	22.8	32.1	52297	16	AAK51411	Mycobacteriophage
c 93	23.6	33.2	421	22	AAK34846	Human adenosine re	c 166	22.8	32.1	52298	14	AAQ47357	L5 mycobacteriopho
c 94	23.6	33.2	488	22	AAK90057	Human polynucleoti	c 167	22.8	32.1	58857	21	AAK58471	Nucleotide sequenc
c 95	23.6	33.2	2156	18	AAK90384	Human MIP-1 alpha/	c 168	22.8	32.1	4403765	22	AAK199683	Mycobacterium tube
c 96	23.6	33.2	2156	21	AAK21258	Human low adenosin	c 169	22.8	32.1	4411529	22	AAK199682	Mycobacterium tube
c 97	23.6	33.2	2156	21	AAK21262	Human low adenosin	c 170	22.8	31.8	650	22	ABK08983	Human IF-gamma rec
c 98	23.6	33.2	2156	21	AAK35136	Human adenosine re	c 171	22.6	31.8	1388	22	AAK59039	Human secreted pro
c 99	23.6	33.2	2156	21	AAK35140	Human adenosine re	c 172	22.6	31.8	1495	15	AAK62695	C-C chemokin rece
c 100	23.6	33.2	6606	21	AAK21265	Human low adenosin	c 173	22.6	31.8	1495	15	AAK62695	Human low adenosin
c 101	23.6	33.2	6606	21	AAK35143	Human adenosine re	c 174	22.6	31.8	1495	21	AAK21264	Human adenosine re
c 102	23.4	33.0	412	21	AAK82265	N. meningitidis pa	c 175	22.6	31.8	1495	21	AAK35142	Human IF-gamma rec
c 103	23.4	33.0	654	22	AAK35513	Human musculoskele	c 176	22.6	31.8	1512	22	AAK61103	Human secreted pro
c 104	23.4	33.0	1199	22	AAK45021	CDNA encoding nove	c 177	22.6	31.8	1560	11	AAK02862	P. putida KT2440-a
c 105	23.4	33.0	1306	22	AAK93806	Human polynucleoti	c 178	22.6	31.8	1760	21	AAK44674	Part of plasmid ps
c 106	23.4	33.0	1933	23	ABLI19239	Human polynucleoti	c 179	22.6	31.8	1812	22	ABK08345	Zea mays DNA fragm
c 107	23.4	33.0	3539	23	ABLI04236	Drosophila melanog	c 180	22.6	31.8	1812	22	AAK99327	Human secreted pro
c 108	23.4	33.0	3921	23	ABLI1097	Drosophila melanog	c 181	22.6	31.8	2253	22	AAK125974	Human protein enco
c 109	23.4	33.0	3933	23	ABLI19238	Drosophila melanog	c 182	22.6	31.8	2442	22	AAK125974	Mutze actin adenyli
c 110	23.4	33.0	4883	22	AAK79410	Human polynucleoti	c 183	22.6	31.8	2556	22	AAK159455	Human polynucleoti
c 111	23.4	33.0	4453	20	AAK23519	Human immune/haema	c 184	22.6	31.8	3438	22	AAK161241	Human polynucleoti
c 112	23.2	32.7	141	19	AAK46281	Human kidney amino	c 185	22.6	31.8	4522	20	AAK35965	Human int-1 mammar
c 113	23.2	32.7	927	20	AAK40856	C. reinhardtii por	c 186	22.6	31.8	5656	22	AAK25976	Mutze ADF promoter
c 114	23.2	32.7	963	22	AAK89281	Human secreted pro	c 187	22.6	31.8	6030	22	AAK25977	Mutze ADF promoter
c 115	23.2	32.7	969	23	AAK84056	Human brain T calc	c 188	22.6	31.8	6030	22	AAK25977	S. erythraea Oleand
c 116	23.2	32.7	1608	23	AAK85253	Pseudomonas aerugi	c 189	22.6	31.8	6939	20	AAK25775	Mutze ADF promoter
c 117	23.2	32.7	1698	23	AAK54133	DNA encoding novel	c 190	22.6	31.8	7728	24	AAK32077	Human immune syste
c 118	23.2	32.7	1838	20	AAK32119	Pseudomonas aerugi	c 191	22.6	31.8	11365	22	AAK73827	Human immune/haema
c 119	23.2	32.7	1838	21	AAK45282	Chlamydomonas rein	c 192	22.6	31.8	13842	21	AAK87297	S. venezuelae macr
c 120	23.2	32.7	1838	22	ABK02866	Chlamydomonas ppo	c 193	22.6	31.8	20046	22	AAK73826	Human immune/haema
c 121	23.2	32.7	3118	22	ABK02863	Human nervous syst	c 194	22.6	31.8	30001	18	AAK61016	Total DNA sequence
c 122	23.2	32.7	3118	22	AAK03980	Human reproductive	c 195	22.6	31.8	30001	19	AAK05110	S. aureofaciens DN
c 123	23.2	32.7	4820	23	ABLI19637	Drosophila melanog	c 196	22.6	31.8	36519	19	AAK22141	Chimpanzee adenovi
c 124	23.2	32.7	6072	22	AAK05085	Genomic sequence #	c 197	22.6	31.8	36778	21	AAK87285	S. venezuelae pik
c 125	23.2	32.7	6072	22	AAK05085	Human reproductive	c 198	22.6	31.8	37948	21	AAK87285	Nucleotide sequenc
c 126	23.2	32.7	6816	24	AAK16826	Human T-type calci	c 199	22.6	31.8	38506	21	AAK75633	Recombinant cosmid
c 127	23.2	32.7	6855	24	AAK16827	Human T-type calci	c 200	22.6	31.8	38506	21	AAK56001	Nucleotide sequenc
c 128	23.2	32.7	6933	23	AAK575141	DNA encoding novel	c 201	22.6	31.8	42717	22	AAK90032	Streptococcus olea
c 129	23.2	32.4	502	19	AAK61336	Extended tumour sp	c 202	22.6	31.8	50937	21	AAK09469	DNA encoding novel
c 130	23.2	32.4	502	19	AAK58665	Prostate tumour sp	c 203	22.6	31.5	420	23	AAK76265	Human breast cance
c 131	23.2	32.4	502	21	AAK06428	Human immunogenic	c 204	22.4	31.5	420	23	AAK76265	Human breast cance
c 132	23.2	32.4	502	21	AAK06428	Human immunogenic	c 205	22.4	31.5	653	22	AAK112793	Human foetal cDNA,
c 133	23.2	32.4	502	22	AAK03656	Human prostate tum	c 206	22.4	31.5	653	22	AAK93997	Human breast cance
c 134	23.2	32.4	502	22	AAK03656	Human prostate tum	c 207	22.4	31.5	683	22	AAK121664	Human polynucleoti
c 135	23.2	32.4	502	22	AAK03656	Human prostate-spe	c 208	22.4	31.5	760	22	AAK121664	Human polynucleoti
c 136	23.2	32.4	502	22	AAK03656	Human prostate-spe	c 209	22.4	31.5	760	22	AAK121664	Human hexose kinas
c 137	23.2	32.4	537	20	AAK87253	Prostate tumour an	c 210	22.4	31.5	1182	21	AAK75608	CDNA encoding a ch
c 138	23.2	32.4	537	20	AAK87253	Prostate tumour an	c 211	22.4	31.5	1182	21	AAK75608	CDNA encoding a ch
c 139	23.2	32.4	1052	22	AAK529788	DNA encoding novel	c 212	22.4	31.5	1452	21	AAK91047	Rat methadone-spec
c 140	23.2	32.4	1052	22	AAK529788	Human cytoskeletal	c 213	22.4	31.5	1574	10	AAK90599	Human lipocortin-V
c 141	23.2	32.4	1310	21	AAK58119	Human PRO1555 (UNO	c 214	22.4	31.5	1695	22	AAK41655	CDNA encoding nove
c 142	23.2	32.4	1310	21	AAK58119	Human PRO1555 (UNO	c 215	22.4	31.5	1695	22	AAK41655	CDNA encoding nove
c 143	23.2	32.4	1362	21	AAK69101	DNA encoding prote	c 216	22.4	31.5	1735	22	AAK45270	CDNA encoding nove
c 144	23.2	32.4	1375	17	AAK04045	Human secreted pro	c 217	22.4	31.5	2953	22	AAK68359	Human immune/haema
c 145	23.2	32.4	1375	17	AAK04045	Human secreted pro	c 218	22.4	31.5	2953	22	AAK68359	Human immune/haema
c 146	23.2	32.4	2001	22	AAK69058	Actinomadura flexu	c 219	22.4	31.5	4226	21	AAK93780	Chicken-pox virus
c 147	23.2	32.4	2001	22	AAK69058	P. putida KT2440-a	c 220	22.4	31.5	4603	22	AAK78076	Human immune/haema
c 148	23.2	32.4	2001	22	AAK69058	Human late stage c	c 221	22.4	31.5	5103	22	AAK61193	Human polynucleoti
c 149	23.2	32.4	6649	23	AAK89518	DNA encoding novel	c 222	22.4	31.5	13744	22	AAK68361	Human immune/haema
c 150	23.2	32.4	6649	23	AAK89518	Human excretory re	c 223	22.4	31.5	13744	22	AAK68361	Human immune/haema
c 151	23.2	32.4	12019	20	AAK18867	Human kidney relat	c 224	22.4	31.5	14049	22	ABK15812	Human nervous syst
c 152	23.2	32.4	349980	20	AAK18867	Alcaligenes sp. po	c 225	22.4	31.5	42519	22	AAK81318	Human immune/haema
c 153	23.2	32.4	349980	20	AAK18867	Alcaligenes sp. po	c 226	22.4	31.5	125157	22	AAK74202	Nucleotide sequenc
c 154	23.2	32.4	349980	20	AAK18867	Alcaligenes sp. po	c 227	22.4	31.5	125157	22	AAK74202	Nucleotide sequenc
c 155	22.8	32.1	549	23	AAK52738	E. coli DNA for ce	c 228	22.2	31.3	338	22	AAK83230	Human polynucleoti

C 229	22.2	31.3	471	22	AAK63647	Human immune/haema	302	22	31.0	124884	22	AAH74201	Nucleotide sequenc
C 230	22.2	31.3	485	22	ABA42253	Human foetal liver	C 303	22	31.0	124884	22	AAH74201	Nucleotide sequenc
C 231	22.2	31.3	485	22	ABA52678	Human foetal liver	C 304	22	31.0	349980	22	AAH68533	C glutamincum codin
C 232	22.2	31.3	485	22	ABA22466	Probe #932 for gen	C 305	21.8	30.7	339	23	AAS69763	DNA encoding novel
C 233	22.2	31.3	485	22	AAK00936	Human brain expres	C 306	21.8	30.7	361	21	AAAB69767	Human ovarian carc
C 234	22.2	31.3	485	22	AAK26390	Human bone marrow	C 307	21.8	30.7	361	21	AAAB69913	Human ovarian carc
C 235	22.2	31.3	485	22	AAI11022	Probe #955 for gen	C 308	21.8	30.7	361	21	AAAB69914	Human ovarian carc
C 236	22.2	31.3	485	22	AAI32284	Probe #970 used to	C 309	21.8	30.7	380	22	ABA45273	Human breast cell
C 237	22.2	31.3	485	22	AAI00942	Probe #933 used to	C 310	21.8	30.7	380	22	ABA25445	Human breast cell
C 238	22.2	31.3	673	21	AAAC9708	Bridge-1 related p	C 311	21.8	30.7	380	22	AAK03983	Human brain expres
C 239	22.2	31.3	682	21	AAAC37215	Arabidopsis thalia	C 312	21.8	30.7	468	22	AAAS2187	Human brain expres
C 240	22.2	31.3	706	20	AAH215277	Human gene express	C 313	21.8	30.7	468	22	AAAS2536	Human ovarian tumo
C 242	22.2	31.3	1215	22	AAH52057	Mycobacterium tube	C 314	21.8	30.7	581	22	AAH83834	Human ovarian tumo
C 243	22.2	31.3	1323	23	AAH85260	DNA encoding novel	C 315	21.8	30.7	647	20	AAH69543	P. neopollyactyla
C 244	22.2	31.3	1343	22	ABA16862	Human nervous syst	C 316	21.8	30.7	647	20	AAH81458	P. gondii immunoge
C 245	22.2	31.3	1343	22	ABA19755	Human nervous syst	C 317	21.8	30.7	647	20	AAH81459	T. gondii ntG647 T
C 246	22.2	31.3	1761	21	AAAB58473	Nucleotide sequenc	C 318	21.8	30.7	647	22	AAH42782	T. gondii CDNA enc
C 247	22.2	31.3	2068	22	ABA20372	Human nervous syst	C 319	21.8	30.7	647	22	AAH42782	Reverse complement
C 248	22.2	31.3	2139	23	AAH54180	Pseudomonas aerugi	C 320	21.8	30.7	860	22	AAH08247	Human cDNA clone (
C 249	22.2	31.3	2547	22	AAH93794	Human cDNA encodin	C 321	21.8	30.7	997	22	AAH94498	Human full-length
C 250	22.2	31.3	2834	8	AAH70307	Sequence of human	C 322	21.8	30.7	1008	22	AAH51988	Mycobacterium tube
C 251	22.2	31.3	2834	10	AAH90394	Genomic DNA of hum	C 323	21.8	30.7	1024	20	AAH33971	Human TIE ligand N
C 252	22.2	31.3	2834	16	AAQ92785	MIS human gene in	C 324	21.8	30.7	1024	21	AAAB0538	Human TIE ligand N
C 253	22.2	31.3	3331	21	AAH75918	Human ORFX ORF1473	C 325	21.8	30.7	1024	22	AAH21401	Human cDNA sequenc
C 254	22.2	31.3	3405	23	AAH76983	DNA encoding novel	C 326	21.8	30.7	1024	22	AAH90565	Human cDNA sequenc
C 255	22.2	31.3	3426	20	AAH23819	Human SRBP-2 CDNA	C 327	21.8	30.7	1024	22	AAH97392	Human PRO198 CDNA
C 256	22.2	31.3	3500	21	AAH74935	Human ORFX ORF490	C 328	21.8	30.7	1029	21	AAH64288	Human angiogenesis
C 257	22.2	31.3	3803	22	AAH60788	Human polynucleoti	C 329	21.8	30.7	1209	20	AAH74286	R. eutropha Mgt OR
C 258	22.2	31.3	3804	22	AAH59002	Human polynucleoti	C 330	21.8	30.7	1211	19	AAH454569	M. vaccae antigen
C 259	22.2	31.3	5197	16	AAQ79038	Human SRBP-2 codi	C 331	21.8	30.7	1211	20	AAH211303	Chimeric PCR decon
C 260	22.2	31.3	5962	23	AAH54522	Pseudophila melanog	C 332	21.8	30.7	1357	21	AAH07486	DNA encoding human
C 261	22.2	31.3	7347	23	AAH54136	Drosophoma aerugi	C 333	21.8	30.7	1471	20	AAH36137	Human diagnostic a
C 262	22.2	31.3	12328	22	AAH20373	Human nervous syst	C 334	21.8	30.7	1508	22	AAH31010	Human secreted pro
C 263	22.2	31.3	23823	22	AAH79160	Human immune/haema	C 335	21.8	30.7	1513	21	AAH39566	Colon cancer assoc
C 264	22.2	31.3	23825	22	AAH79161	Human immune/haema	C 336	21.8	30.7	1898	20	AAH40075	DNA encoding novel
C 265	22.2	31.3	35048	23	ABL06102	Drosophila melanog	C 337	21.8	30.7	1898	23	AAH66871	Escherichia coli p
C 266	22.2	31.3	4411529	22	AAH96862	Mycobacterium tube	C 338	21.8	30.7	2129	22	AAH88920	Human protein kina
C 267	22.2	31.0	653	21	AAH06588	Human immunogenic	C 339	21.8	30.7	2191	21	AAH88502	Human polynucleoti
C 268	22.2	31.0	653	22	AAH63797	Human prostate CDN	C 340	21.8	30.7	2524	22	AAH82863	Human polynucleoti
C 269	22.2	31.0	653	22	AAH93704	Human prostate-spe	C 341	21.8	30.7	2531	22	AAH51879	Human polynucleoti
C 270	22.2	31.0	653	22	AAH85018	Human prostate-spe	C 342	21.8	30.7	2625	22	AAH26354	P. putida oxygenas
C 271	22.2	31.0	713	21	AAH02769	Prostate tumour an	C 343	21.8	30.7	2801	22	AAH26992	CDNA encoding nove
C 272	22.2	31.0	713	21	AAH08097	Hepatitis type C v	C 344	21.8	30.7	3397	22	AAH60273	Human polynucleoti
C 273	22.2	31.0	734	22	AAH07713	Human cDNA clone (	C 345	21.8	30.7	3510	23	AAH66874	DNA encoding novel
C 274	22.2	31.0	792	12	AAH48413	Arabidopsis thalia	C 346	21.8	30.7	3557	22	AAH83109	HOSR-1 ovarian tum
C 275	22.2	31.0	836	12	AAH012218	SMUC-41 intestinal	C 347	21.8	30.7	3557	22	AAH818639	Human cDNA sequenc
C 276	22.2	31.0	1104	23	ABL26081	Drosophila melanog	C 348	21.8	30.7	3557	22	AAH818639	Human matrix-type
C 277	22.2	31.0	1134	23	AAH68035	C glutamincum codin	C 349	21.8	30.7	3991	24	AAH16274	CDNA encoding chic
C 278	22.2	31.0	1641	23	AAH73131	DNA encoding novel	C 350	21.8	30.7	4037	23	AAH69666	DNA encoding novel
C 279	22.2	31.0	1754	22	AAH14926	Human cDNA sequenc	C 351	21.8	30.7	4142	19	AAH62750	Human secreted pro
C 280	22.2	31.0	2307	22	AAH59307	Human polynucleoti	C 352	21.8	30.7	4326	23	AAH69668	DNA encoding novel
C 281	22.2	31.0	2888	22	ABL16825	Drosophila melanog	C 353	21.8	30.7	5751	22	AAH51986	Human polynucleoti
C 282	22.2	31.0	2898	22	AAH60867	Human cancer agent	C 354	21.8	30.7	7539	22	AAH158487	Human polynucleoti
C 283	22.2	31.0	2898	22	AAH60868	Human cancer agent	C 355	21.8	30.7	7620	22	AAH07349	Human pancreatic c
C 284	22.2	31.0	3170	23	ABL26080	Drosophila melanog	C 356	21.8	30.7	7620	22	AAH32776	Human genomic DNA
C 285	22.2	31.0	3294	22	AAH57441	Human intestine ce	C 357	21.8	30.7	9549	22	AAH53175	Human purified sec
C 286	22.2	31.0	4011	15	AAH070362	Varicella zoster v	C 358	21.8	30.7	15355	22	AAH57405	Human skeletal mus
C 287	22.2	31.0	4011	15	AAH066981	DNA encoding VZV 1	C 359	21.8	30.7	15359	22	AAH08724	Human tyandoline re
C 288	22.2	31.0	6114	20	AAH83490	Human T-type volta	C 360	21.8	30.7	15359	22	AAH83490	DNA encoding novel
C 289	22.2	31.0	6132	20	AAH83489	Human T-type volta	C 361	21.8	30.7	15464	12	AAH11415	Ryanodine receptor
C 290	22.2	31.0	6690	23	ABL16769	Drosophila melanog	C 362	21.8	30.7	16026	22	AAH16260	Human nervous syst
C 291	22.2	31.0	7549	22	AAH32737	Human genomic DNA	C 363	21.8	30.7	17514	22	AAH85026	Human immune/haema
C 292	22.2	31.0	7549	22	AAH32738	Human genomic DNA	C 364	21.8	30.7	18522	23	AAH59560	Propionibacterium
C 293	22.2	31.0	9839	22	AAH99052	Human excretory re	C 365	21.8	30.7	19115	22	ABA16261	Human nervous syst
C 294	22.2	31.0	9968	22	AAH16353	Human kidney relat	C 366	21.8	30.7	30690	21	AAH92301	S. avermilitis ave
C 295	22.2	31.0	15720	22	AAH129504	Human musculoskele	C 367	21.8	30.7	30690	22	AAH92777	Streptomyces averm
C 296	22.2	31.0	19861	22	AAH71206	C899P determined c	C 368	21.8	30.7	37716	23	AAH90655	Propionibacterium
C 297	22.2	31.0	29139	23	AAH59569	Human immune/haema	C 369	21.6	30.4	504	22	AAH90700	Human MANGO 349 cD
C 298	22.2	31.0	47670	23	AAH59569	Propionibacterium	C 370	21.6	30.4	504	22	AAH90700	Human MANGO 349 cD
C 299	22.2	31.0	50368	23	ABL16824	Drosophila melanog	C 371	21.6	30.4	504	22	AAH90702	Human MANGO 349 R2
C 300	22.2	31.0	50937	21	AAH09469	Drosophila melanog	C 372	21.6	30.4	504	22	AAH90702	Human MANGO 349 R2
C 301	22.2	31.0	109519	22	AAH08693	Streptococcus olea	C 373	21.6	30.4	504	22	AAH90703	Human MANGO 349 E4
						Micromonospora DNA	C 374	21.6	30.4	565	21	AAH08704	Fusarium venenatum

C 375	21.6	30.4	566	22	AAH10007	Human cDNA clone (	C 448	21.4	30.1	566	22	ABA31339	Probe #9805 for ge
C 376	21.6	30.4	630	23	ABLO6637	Drosophila melanog	C 449	21.4	30.1	566	22	AAK12668	Human brain expres
C 377	21.6	30.4	679	22	AAH16843	Human cDNA clone (	C 450	21.4	30.1	566	22	AAK38385	Human bone marrow
C 378	21.6	30.4	801	22	AA197433	Human neuroblastom	C 451	21.4	30.1	566	22	AA119182	Probe #9115 for ge
C 379	21.6	30.4	880	21	AA267178	Candida albicans p	C 452	21.4	30.1	566	22	AA144340	Probe #13026 used
C 380	21.6	30.4	903	23	AA583666	DNA encoding novel	C 453	21.4	30.1	573	18	AAV06338	Recombinant protei
C 381	21.6	30.4	903	23	AA592437	DNA encoding novel	C 454	21.4	30.1	696	21	AAE12111	Aspergillus oryzae
C 382	21.6	30.4	1027	14	AA043452	Sequence of endoce	C 455	21.4	30.1	750	23	AA580936	DNA encoding novel
C 383	21.6	30.4	1032	21	AA112986	DNA encoding strep	C 456	21.4	30.1	888	22	AAK86183	Human immune/haema
C 384	21.6	30.4	1212	22	AA523237	DNA encoding novel	C 457	21.4	30.1	1016	17	AA729401	Lipase coding sequ
C 385	21.6	30.4	1422	22	AA523150	DNA encoding novel	C 458	21.4	30.1	1027	23	AA568733	DNA encoding novel
C 386	21.6	30.4	1548	20	AA520523	Poly nucleotide seq	C 459	21.4	30.1	1027	23	AA568733	DNA encoding novel
C 387	21.6	30.4	1549	16	AAQ88151	Xanthomonas L-glut	C 460	21.4	30.1	1176	21	AAE78151	Human tumour supp
C 388	21.6	30.4	1791	21	AA562454	CDNA sequence #241	C 461	21.4	30.1	1176	21	AAE78151	Human tumour assoc
C 389	21.6	30.4	1831	21	AA27487	5' HB5 endogenous r	C 462	21.4	30.1	1368	23	ABLO2939	Drosophila melanog
C 390	21.6	30.4	1958	22	AAH18689	Human cDNA sequenc	C 463	21.4	30.1	1541	22	AA59774	Propionibacterium
C 391	21.6	30.4	2006	15	AA050147	Human cDNA sequenc	C 464	21.4	30.1	1541	22	AA59774	Human aldehyde deh
C 392	21.6	30.4	2110	20	AAV84610	Human secreted pro	C 465	21.4	30.1	1541	22	AAH14702	Human cDNA sequenc
C 393	21.6	30.4	2110	22	AB883393	Human secreted pro	C 466	21.4	30.1	1551	24	AB134326	Human immune syste
C 394	21.6	30.4	2255	21	AA72387	Human nucleic acid	C 467	21.4	30.1	1709	22	AAK51755	DNA encoding novel
C 395	21.6	30.4	2281	22	AAE98709	Human late stage o	C 468	21.4	30.1	1851	23	AA582716	DNA encoding novel
C 396	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 469	21.4	30.1	1873	22	AAK94604	Human full-length
C 397	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 470	21.4	30.1	1945	22	AAK52739	Human polynucleoti
C 398	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 471	21.4	30.1	2036	20	AAK52739	Human breast tumo
C 399	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 472	21.4	30.1	2036	20	AAK52739	Lung cancer associ
C 400	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 473	21.4	30.1	2036	20	AAK52739	Human keratin KRT
C 401	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 474	21.4	30.1	2036	20	AAK52739	Human shear stress
C 402	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 475	21.4	30.1	2036	20	AAK52739	Human secreted pro
C 403	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 476	21.4	30.1	2036	20	AAK52739	Human secreted pro
C 404	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 477	21.4	30.1	2036	20	AAK52739	M. tuberculosis an
C 405	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 478	21.4	30.1	2036	20	AAK52739	Mycobacterium tube
C 406	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 479	21.4	30.1	2036	20	AAK52739	Human secreted pro
C 407	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 480	21.4	30.1	2036	20	AAK52739	C glutamic acid cod
C 408	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 481	21.4	30.1	2036	20	AAK52739	Human immune/haema
C 409	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 482	21.4	30.1	2036	20	AAK52739	Pseudomonas aerugi
C 410	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 483	21.4	30.1	2036	20	AAK52739	Rat glycine transp
C 411	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 484	21.4	30.1	2036	20	AAK52739	Human cDNA sequenc
C 412	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 485	21.4	30.1	2036	20	AAK52739	Nucleotide sequenc
C 413	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 486	21.4	30.1	2036	20	AAK52739	Human diagnostic a
C 414	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 487	21.4	30.1	2036	20	AAK52739	Human nervous syst
C 415	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 488	21.4	30.1	2036	20	AAK52739	SEQ ID 6 of W09919
C 416	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 489	21.4	30.1	2036	20	AAK52739	DNA encoding novel
C 417	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 490	21.4	30.1	2036	20	AAK52739	Drosophila melanog
C 418	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 491	21.4	30.1	2036	20	AAK52739	Drosophila melanog
C 419	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 492	21.4	30.1	2036	20	AAK52739	CDNA encoding huma
C 420	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 493	21.4	30.1	2036	20	AAK52739	Human reproductive
C 421	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 494	21.4	30.1	2036	20	AAK52739	Human activated ca
C 422	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 495	21.4	30.1	2036	20	AAK52739	Human activated ca
C 423	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 496	21.4	30.1	2036	20	AAK52739	Human activated ca
C 424	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 497	21.4	30.1	2036	20	AAK52739	Human activated ca
C 425	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 498	21.4	30.1	2036	20	AAK52739	Human immune/haema
C 426	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 499	21.4	30.1	2036	20	AAK52739	Human immune/haema
C 427	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 500	21.4	30.1	2036	20	AAK52739	Genomic sequence #
C 428	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 501	21.4	30.1	2036	20	AAK52739	Human nervous syst
C 429	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 502	21.4	30.1	2036	20	AAK52739	Human nervous syst
C 430	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 503	21.4	30.1	2036	20	AAK52739	Human immune/haema
C 431	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 504	21.4	30.1	2036	20	AAK52739	Human immune/haema
C 432	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 505	21.4	30.1	2036	20	AAK52739	Human corticostero
C 433	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 506	21.4	30.1	2036	20	AAK52739	Human immune/haema
C 434	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 507	21.4	30.1	2036	20	AAK52739	Amycolatopsis medi
C 435	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 508	21.4	30.1	2036	20	AAK52739	Nucleotide sequenc
C 436	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 509	21.4	30.1	2036	20	AAK52739	Human adenosine Al
C 437	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 510	21.4	30.1	2036	20	AAK52739	C glutamic acid cod
C 438	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 511	21.4	30.1	2036	20	AAK52739	Human silent SNP c
C 439	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 512	21.4	30.1	2036	20	AAK52739	Exon-intron repair co
C 440	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 513	21.4	30.1	2036	20	AAK52739	Human brain expres
C 441	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 514	21.4	30.1	2036	20	AAK52739	Human secreted pro
C 442	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 515	21.4	30.1	2036	20	AAK52739	DNA encoding novel
C 443	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 516	21.4	30.1	2036	20	AAK52739	DNA encoding novel
C 444	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 517	21.4	30.1	2036	20	AAK52739	Murine 7-transmemb
C 445	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 518	21.4	30.1	2036	20	AAK52739	Human cDNA clone (
C 446	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 519	21.4	30.1	2036	20	AAK52739	DNA encoding novel
C 447	21.6	30.4	2286	20	AA501152	M. tuberculosis an	C 520	21.4	30.1	2036	20	AAK52739	Human immune/haema

521	21.2	29.9	639	23	AA575935	DNA encoding novel	594	21.2	29.9	37736	22	AAK86139	Human immune/haema
522	21.2	29.9	660	20	AA586008	DNA encoding a gyr	595	21.2	29.9	65140	22	AAD17184	Streptomyces nous
523	21.2	29.9	677	21	AA513916	Aspergillus oryzae	596	21.2	29.9	125401	22	AAD17186	Streptomyces nous
524	21.2	29.9	701	16	AAO76209	HSV L/ST ORF1. He	597	21.2	28.9	534720	19	AAV30458	Rhizobium species
525	21.2	29.9	712	22	AA531514	Human DNA for a no	598	21.2	29.9	536165	19	AAV30459	Rhizobium species
526	21.2	29.9	747	22	AA508464	Fusarium venenatu	599	21.2	29.9	1830121	17	AA742063	Haemophilus Influe
527	21.2	29.9	792	22	AA196336	Human neuroblastom	600	21	29.6	141	22	AAK24431	Human foetal expres
528	21.2	29.9	801	22	AA197509	Human neuroblastom	601	21	29.6	158	22	ABA75016	Human foetal liver
529	21.2	29.9	847	22	AA160675	Human polynucleoti	602	21	29.6	158	22	ABA39703	Probe #18169 for g
530	21.2	29.9	857	22	AA120041	Human breast cance	603	21	29.6	158	22	AAK23526	Human brain expres
531	21.2	29.9	906	21	AAA26407	Human secreted pro	604	21	29.6	158	22	AAK49658	Human bone marrow
532	21.2	29.9	910	22	AA158889	Human polynucleoti	605	21	29.6	158	22	AAK126766	Probe #16699 for g
533	21.2	29.9	953	22	AA510662	Rat GFRA1pha-4 spl	606	21	29.6	158	22	AA155543	Probe #24229 used
534	21.2	29.9	1008	22	AA531063	Rat GFRA1pha-4 spl	607	21	29.6	279	20	AA89544	EST clone CR1135.
535	21.2	29.9	1023	23	AA554245	Pseudomonas aerugi	608	21	29.6	297	20	AA615559	Genetic suppressor
536	21.2	29.9	1074	23	AA571558	DNA encoding novel	609	21	29.6	351	21	AA258778	Human huntingtin-1
537	21.2	29.9	1248	22	AA590937	Human I-beta-1,3-N	610	21	29.6	373	21	AA661555	Genetic suppressor
538	21.2	29.9	1256	23	AB105853	Drosophila melanog	611	21	29.6	386	22	AA565986	Novel human polynu
539	21.2	29.9	1281	21	AAA64852	Bordetella pertuss	612	21	29.6	400	22	AA565738	Novel human polynu
540	21.2	29.9	1446	23	AB113517	Drosophila melanog	613	21	29.6	423	21	AA615562	Genetic suppressor
541	21.2	29.9	1461	22	AA594439	Human hydrophobic	614	21	29.6	423	21	AA313674	Plant microsatelli
542	21.2	29.9	1593	22	AA591989	Murine T-bet codin	615	21	29.6	432	22	AAH34220	Human colon cancer
543	21.2	29.9	1608	22	AA591988	Human T-bet codin	616	21	29.6	442	22	AAH12073	Human nervous syst
544	21.2	29.9	1722	23	AA580551	DNA encoding novel	617	21	29.6	492	21	AA575840	Human OREF ORF1395
545	21.2	29.9	1728	23	AA552506	E. coli DNA for ce	618	21	29.6	502	22	ABA82610	Human Zmax 1 PCR p
546	21.2	29.9	1735	22	AA104953	Human reproductive	619	21	29.6	524	21	AA661554	Genetic suppressor
547	21.2	29.9	1758	22	AA594449	Human hydrophobic	620	21	29.6	531	22	ABA62493	Human foetal liver
548	21.2	29.9	1923	22	AA559861	Human novel cytol	621	21	29.6	531	22	ABA29824	Probe #4290 for ge
549	21.2	29.9	1940	22	AA594497	Human novel cytol	622	21	29.6	531	22	AAK10844	Human brain expres
550	21.2	29.9	1968	21	AA556211	Salmonella typhi D	623	21	29.6	531	22	AAK36706	Human bone marrow
551	21.2	29.9	2011	20	AA599465	Beta 1,3-N-acetyl	624	21	29.6	531	22	AA117559	Probe #1792 for ge
552	21.2	29.9	2019	23	AA593188	DNA encoding novel	625	21	29.6	531	22	AA142472	Probe #1158 used
553	21.2	29.9	2175	22	AA558449	Mitomycin biosynth	626	21	29.6	535	22	AAK11847	Human brain expres
554	21.2	29.9	2175	22	AA596644	Mitomycin biosynth	627	21	29.6	535	22	AAK11847	Human brain expres
555	21.2	29.9	2214	17	AA528807	Mitomycin biosynth	628	21	29.6	535	22	AAK11847	Human brain expres
556	21.2	29.9	2385	21	AA539981	Human G-protein co	629	21	29.6	630	21	AA550089	Human breast cance
557	21.2	29.9	2413	22	AA515635	Human TANGO 187 cd	630	21	29.6	641	23	AA577094	Human breast cance
558	21.2	29.9	2418	21	AA539979	Human cDNA sequenc	631	21	29.6	687	23	AA577094	Human breast cance
559	21.2	29.9	2464	22	AA539979	Human TANGO 187-2	632	21	29.6	736	21	AA583337	Human polynucleoti
560	21.2	29.9	2490	21	AA539975	Human cDNA sequenc	633	21	29.6	736	21	AA583337	DNA encoding novel
561	21.2	29.9	2523	21	AA539978	Human TANGO 187-1	634	21	29.6	783	17	AA583337	DNA encoding novel
562	21.2	29.9	2524	21	AA539978	Human TANGO 187-1	635	21	29.6	823	23	AA583337	31-O-desmethyl-FK5
563	21.2	29.9	2552	24	AA599908	Polynucleotide enc	636	21	29.6	940	22	AA109960	Aspergillus oryzae
564	21.2	29.9	2595	21	AA539980	Human TANGO 187-3	637	21	29.6	1001	21	AA581516	Human breast cance
565	21.2	29.9	2639	14	AA539976	Human TANGO 187-2	638	21	29.6	1066	22	AA190707	Human polynucleoti
566	21.2	29.9	2639	15	AA539977	2,2-dialkylglycine	639	21	29.6	1082	23	AA565697	DNA encoding novel
567	21.2	29.9	2700	21	AA539977	Dialkylglycine dec	640	21	29.6	1150	17	AA503650	31-O-desmethyl-FK5
568	21.2	29.9	3219	23	AA574721	Human TANGO 187-1	641	21	29.6	1242	23	AA572110	DNA encoding novel
569	21.2	29.9	3267	23	AB117571	Drosophila melanog	642	21	29.6	1425	23	AB103085	Drosophila melanog
570	21.2	29.9	3567	23	AB113516	Drosophila melanog	643	21	29.6	1604	21	AA251983	Mouse Plox2b nucle
571	21.2	29.9	4157	23	AB106835	Drosophila melanog	644	21	29.6	1806	22	ABA15719	Human nervous syst
572	21.2	29.9	4424	22	AAK51737	Drosophila melanog	645	21	29.6	1854	20	AAK32296	Human nervous syst
573	21.2	29.9	4504	22	AAK52721	Human polynucleoti	646	21	29.6	1960	20	AA220931	M. grisea PTH11 ge
574	21.2	29.9	5519	20	AA524982	Haemophilus influe	647	21	29.6	1962	20	AA220932	Human MUC18 cDNA s
575	21.2	29.9	5561	20	AA524981	Haemophilus influe	648	21	29.6	1971	22	AA251983	Human MUC18 cDNA s
576	21.2	29.9	5561	20	AA524981	Haemophilus influe	649	21	29.6	1971	22	AA251983	C glutaminc codin
577	21.2	29.9	6943	22	AA542087	Drosophila melanog	650	21	29.6	2086	22	AA527113	CDNA encoding nove
578	21.2	29.9	7029	24	AA517119	Genomic sequence #	651	21	29.6	2265	21	AA545625	Arabidopsis thalia
579	21.2	29.9	7312	23	AB105852	Ketoglucuronidase	652	21	29.6	2271	23	AA586441	DNA encoding novel
580	21.2	29.9	8011	23	AB106834	Drosophila melanog	653	21	29.6	2361	22	AA527490	DNA encoding nove
581	21.2	29.9	9045	22	AA506332	DNA encoding seven	654	21	29.6	2397	21	AA246408	Asb2ya gossypii is
582	21.2	29.9	9087	22	AA514986	Human NOV7 DNA. H	655	21	29.6	2475	22	AAH84578	Aspergillus oryzae
583	21.2	29.9	11389	22	AA559825	Human novel cytol	656	21	29.6	2547	14	AAO372238	E. coli growth and
584	21.2	29.9	11604	22	AA514501	Streptomyces clavu	657	21	29.6	2651	20	AAO372238	C. melassaccola ATCC
585	21.2	29.9	11839	23	AB114261	Drosophila melanog	658	21	29.6	2686	22	AA513465	Human HCMV Inducib
586	21.2	29.9	12001	16	AAO76213	HSV L/ST region.	659	21	29.6	2720	19	AA510464	DNA encoding human
587	21.2	29.9	15044	22	AA536290	Human cardiovascular	660	21	29.6	2835	22	AAK86547	S. capsulata proly
588	21.2	29.9	15046	22	AA536291	Human cardiovascular	661	21	29.6	2887	21	AA599014	Human immune/haema
589	21.2	29.9	15079	16	AAO91580	S. clavuligerus cl	662	21	29.6	2949	23	AA567904	DNA encoding novel
590	21.2	29.9	15079	16	AAO91580	S. clavuligerus cl	663	21	29.6	2949	23	AA567904	DNA encoding novel
591	21.2	29.9	18034	21	AA55841	Streptomyces clavu	664	21	29.6	3215	22	AA558320	Human GTP-binding
592	21.2	29.9	23333	23	AB114260	Complete Mitomycin	665	21	29.6	3247	22	AAD11946	Human protein phos
593	21.2	29.9	35026	21	AA564890	Bordetella pertuss	666	21	29.6	3293	22	AAH02921	Human shear stress

C 667	21	29.6	3437	22	AAK5235	Human polynucleoti	114	740	20.8	29.3	114	22	AAI10241	Human breast cancer
C 668	21	29.6	3787	23	AAK84930	DNA encoding novel	741	741	20.8	29.3	114	22	AAI19821	Human breast cancer
C 669	21	29.6	3835	20	AAK32295	M. grisea PH11 ge	742	742	20.8	29.3	125	22	AAI20499	Human breast cancer
C 670	21	29.6	4281	24	AAK971177	Human metalloprote	743	743	20.8	29.3	132	22	AAH67315	C glutamicum codin
C 671	21	29.6	4351	19	AAV70397	LRP5 isoform 2 lon	744	744	20.8	29.3	140	22	AAH11601	Human breast cancer
C 672	21	29.6	4509	20	AAZ30081	cDNA encoding a hu	745	745	20.8	29.3	164	21	AAV12042	Human secreted pro
C 673	21	29.6	4511	22	AAAD16259	Human ATP-binding	746	746	20.8	29.3	324	19	AAV11442	Nucleotide sequenc
C 674	21	29.6	4512	22	AAAD16231	Human ATP-binding	747	747	20.8	29.3	324	22	AAK98414	5' portion of cDNA
C 675	21	29.6	4512	22	AAAD16256	Human ATP-binding	748	748	20.8	29.3	362	22	AAI80095	Human polynucleoti
C 676	21	29.6	4512	22	AAAD16257	Human ATP-binding	749	749	20.8	29.3	381	20	AAV86329	EST clone AJ158.
C 677	21	29.6	4512	22	AAAD16260	Human ATP-binding	750	750	20.8	29.3	406	22	AAK64514	Novel human polyu
C 678	21	29.6	4512	22	AAAD16261	Human ATP-binding	751	751	20.8	29.3	452	21	AAK00562	Novel human polyu
C 679	21	29.6	4512	22	AAAD16261	Human ATP-binding	752	752	20.8	29.3	540	21	AAK42316	Human secreted exp
C 680	21	29.6	4512	22	AAAD16262	Human ATP-binding	753	753	20.8	29.3	560	22	AAK36173	Human cardiovascul
C 681	21	29.6	4512	22	AAAD16263	Human ATP-binding	754	754	20.8	29.3	572	20	AAV80572	Nucleic acid seq I
C 682	21	29.6	4512	22	AAAD16264	Human ATP-binding	755	755	20.8	29.3	585	22	AAK92939	Human cDNA 3'-end
C 683	21	29.6	4795	20	AAK32297	M. grisea PH12 ge	756	756	20.8	29.3	627	22	AAH67316	C glutamicum codin
C 684	21	29.6	4843	19	AAV70395	LRP5 cDNA longest	757	757	20.8	29.3	643	20	AAK08685	Novel nucleotide s
C 685	21	29.6	4896	22	AAI59468	Human polynucleoti	758	758	20.8	29.3	650	16	AAV01589	Rat neu promoter.
C 686	21	29.6	4915	19	AAV70398	LRP5 isoform 3 put	759	759	20.8	29.3	655	19	AAV11431	Human secreted pro
C 687	21	29.6	5021	21	AAZ46407	Aspergillus oryzae	760	760	20.8	29.3	730	22	AAH03566	Human cDNA clone (
C 688	21	29.6	5022	19	AAK85549	LRP5 isoform 5 cDN	761	761	20.8	29.3	756	21	AAH51433	Human UGT1A7 relat
C 689	21	29.6	5098	22	AAV70396	Human calcium chan	762	762	20.8	29.3	804	22	AAK80289	Human immune/haema
C 690	21	29.6	5120	22	AAK82617	Human Zmax1 gene S	763	763	20.8	29.3	951	21	AAH51432	Human UGT1A7 relat
C 691	21	29.6	5120	22	AAK82618	Human HBM gene SEQ	764	764	20.8	29.3	968	22	AAK52243	Human cDNA encodin
C 692	21	29.6	5125	19	AAV86019	LRP5 isoform 3 cDN	765	765	20.8	29.3	1035	22	AAK52279	Human cDNA encodin
C 693	21	29.6	5263	19	AAV70400	LRP5 isoform 4 cDN	766	766	20.8	29.3	1065	23	AAK94423	Human hydrophobic
C 694	21	29.6	5438	13	AAQ29263	Human calcium chan	767	767	20.8	29.3	1134	23	AAK593484	DNA encoding novel
C 695	21	29.6	6114	23	AAK59640	Protonlactactium	768	768	20.8	29.3	1167	22	AAK122751	Drosophila melanog
C 696	21	29.6	6863	21	AACT4847	Human ORFX ORF402	769	769	20.8	29.3	1167	22	AAK81355	Quorum sensing com
C 697	21	29.6	7286	17	AAU14547	Cytactactin gene.	770	770	20.8	29.3	1170	13	AAQ20217	Sequence of tuf3 g
C 698	21	29.6	7246	20	AAK77924	Human tenascin cDN	771	771	20.8	29.3	1195	21	AAK49878	Arabidopsis thalia
C 699	21	29.6	7560	22	AAK83437	Human tenascin-C.	772	772	20.8	29.3	1198	21	AAK33286	Arabidopsis thalia
C 700	21	29.6	7943	22	AAK83418	Human immune/haema	773	773	20.8	29.3	1233	22	AAH44089	Oryza sativa perox
C 701	21	29.6	8115	22	ABAI6258	Human nervous syst	774	774	20.8	29.3	1283	21	AAK18288	Lung cancer associ
C 702	21	29.6	8910	23	ABLO3395	Drosophila melanog	775	775	20.8	29.3	1300	15	AAO77979	Nontranslocated el
C 703	21	29.6	9466	23	ABLO3084	Drosophila melanog	776	776	20.8	29.3	1368	18	AAK66463	Thermophilic alkali
C 704	21	29.6	9733	22	AAAL04202	Human reproductive	777	777	20.8	29.3	1400	21	AAK65448	Porcine BAC-PIGF2-
C 705	21	29.6	9738	22	AAAL04203	Human reproductive	778	778	20.8	29.3	1521	16	AAK085043	3-Hydroxysteroid-o
C 706	21	29.6	14061	23	ABLO3394	Drosophila melanog	779	779	20.8	29.3	1521	17	AAK62676	3-Hydroxysteroid o
C 707	21	29.6	14652	21	AAAH1482	N. meningitidis pa	780	780	20.8	29.3	1521	19	AAV11824	Streptomyces sp. s
C 708	21	29.6	15254	22	AAK83135	Human immune/haema	781	781	20.8	29.3	1524	18	AAK63517	Xylanase gene obta
C 709	21	29.6	15254	22	AAK83137	Human immune/haema	782	782	20.8	29.3	1524	22	AAK63517	Pseudomonas sp hea
C 710	21	29.6	15255	22	AAK83136	Human immune/haema	783	783	20.8	29.3	1542	22	AAK5141	Human Immune/haema
C 711	21	29.6	15256	22	AAK83134	Human immune/haema	784	784	20.8	29.3	1543	22	AAH13768	Human cDNA sequenc
C 712	21	29.6	16499	22	AAK77656	Human immune/haema	785	785	20.8	29.3	1647	16	AAK085042	3-Hydroxysteroid-o
C 713	21	29.6	18660	21	AAAS8472	Human immune/haema	786	786	20.8	29.3	1647	17	AAK62675	3-Hydroxysteroid o
C 714	21	29.6	21358	22	AAAS39919	Nucleotide sequenc	787	787	20.8	29.3	1647	19	AAV11823	Streptomyces sp. s
C 715	21	29.6	21358	22	AAAL06419	Genomic sequence #	788	788	20.8	29.3	1719	24	ABK04219	Human xylose isom
C 716	21	29.6	21358	22	AAK73090	Human reproductive	789	789	20.8	29.3	1734	14	AAK040428	Human xylose isom
C 717	21	29.6	21358	22	AAK87446	Human immune/haema	790	790	20.8	29.3	1734	14	AAK040429	Hepatitis C virus
C 718	21	29.6	21358	22	AAK87558	Human immune/haema	791	791	20.8	29.3	1734	14	AAK040430	Hepatitis C virus
C 719	21	29.6	21358	22	AAK87563	Human immune/haema	792	792	20.8	29.3	1734	14	AAK040430	Hepatitis C virus
C 720	21	29.6	21632	22	AAAS42019	Human digestive sy	793	793	20.8	29.3	1734	14	AAK040437	Hepatitis C virus
C 721	21	29.6	21676	22	AAK38918	Genomic sequence #	794	794	20.8	29.3	1751	15	AAK040438	Hepatitis C virus
C 722	21	29.6	21676	22	AAAL06418	Genomic sequence #	795	795	20.8	29.3	1839	22	AAK071193	Clavulanic acid re
C 723	21	29.6	21676	22	AAK73081	Human reproductive	796	796	20.8	29.3	1839	22	AAK071193	Human excretory re
C 724	21	29.6	21676	22	AAK87445	Human immune/haema	797	797	20.8	29.3	1865	16	AAK085047	Human kidney relat
C 725	21	29.6	21676	22	AAK87549	Human immune/haema	798	798	20.8	29.3	1865	16	AAK085047	3-Hydroxysteroid-o
C 726	21	29.6	21676	22	AAK87549	Human immune/haema	799	799	20.8	29.3	1865	19	AAK62674	3-Hydroxysteroid o
C 727	21	29.6	21948	20	AAK20562	Human digestive sy	800	800	20.8	29.3	1901	23	AAK71980	Streptomyces sp. s
C 728	21	29.6	27541	22	AAAD17185	Polynucleotide seq	801	801	20.8	29.3	2001	22	AAK71980	DNA encoding novel
C 729	21	29.6	27666	23	ABLO8332	Streptomyces nous	802	802	20.8	29.3	2082	22	AAK71980	Human hydropobic
C 730	21	29.6	30078	21	AAAH1520	Drosophila melanog	803	803	20.8	29.3	2091	23	AAK71980	Human cDNA sequenc
C 731	21	29.6	30078	21	AAAH1520	N. meningitidis pa	804	804	20.8	29.3	2150	20	AAK71980	DNA encoding novel
C 732	21	29.6	30078	21	AAAH1520	Nucleotide sequenc	805	805	20.8	29.3	2153	22	AAK71980	Mouse N-acetylgluc
C 733	21	29.6	107820	22	AAAD16230	Human ATP-binding	806	806	20.8	29.3	2159	22	AAK71980	Human immune/haema
C 734	21	29.6	122186	22	AAK89560	Human histone deac	807	807	20.8	29.3	2159	22	AAK71980	Human excretory re
C 735	21	29.6	125401	22	AAAD17186	Streptomyces nous	808	808	20.8	29.3	2163	20	AAK71980	Human kidney relat
C 736	21	29.6	309400	22	AAH68534	C glutamicum codin	809	809	20.8	29.3	2163	20	AAK71980	B. fragilis DNA pr
C 737	21	29.6	349980	21	AAK21608	Neisseria meningit	810	810	20.8	29.3	2261	22	AAK71980	Cholesterol oxid
C 738	21	29.6	837096	21	AAK21611	Neisseria meningit	811	811	20.8	29.3	2261	22	AAK71980	Human immune/haema
C 739	21	29.6	1437668	21	AAAH1481	N. meningitidis pa	812	812	20.8	29.3	2280	22	AAK71980	cDNA sequence #93
					AAAH1481	N. meningitidis B							AAH160332	Human polynucleoti



C 813	20.8	29.3	2341	22	AAI58536	Human polynucleotidi
C 814	20.8	29.3	2368	22	AA541588	cDNA encoding nove
C 815	20.8	29.3	2380	22	AAFP4433	Human hydrophobic
C 816	20.8	29.3	2420	21	AAZ46489	PKA substrate, Csk
C 817	20.8	29.3	2429	23	ABLI2674	Drosophila melanog
C 818	20.8	29.3	2466	23	AAI93804	Human polynucleoti
C 819	20.8	29.3	2488	23	ABLI17627	Drosophila melanog
C 820	20.8	29.3	2496	23	AA523013	DNA encoding novel
C 821	20.8	29.3	2653	21	AAAD00572	Human Hscd6 cDNA.
C 822	20.8	29.3	2694	22	AAFP4452	Human hydrophobic
C 823	20.8	29.3	2732	22	AA508630	Human cDNA (DMA148
C 824	20.8	29.3	2735	22	AA541048	cDNA encoding nove
C 825	20.8	29.3	2774	18	AAAT9535	Human DNA replicat
C 826	20.8	29.3	2777	22	AA508632	Human cDNA (DMA148
C 827	20.8	29.3	3159	21	AA594964	Human DNA encoding
C 828	20.8	29.3	3166	22	AA522919	DNA encoding novel
C 829	20.8	29.3	3202	23	ABLI22750	Drosophila melanog
C 830	20.8	29.3	3400	21	AAAC76598	Human ORFX ORF2153
C 831	20.8	29.3	3830	8	AAAT70938	DNA fragment contig
C 832	20.8	29.3	4167	22	ABA08224	Human ovarian and
C 833	20.8	29.3	4167	22	AA529236	Genomic sequence #
C 834	20.8	29.3	4167	22	AA530018	Human lung antigen
C 835	20.8	29.3	4167	22	AAI05022	Human reproductive
C 836	20.8	29.3	4167	22	AAI07543	Human reproductive
C 837	20.8	29.3	4167	22	AA528711	Genomic sequence #
C 838	20.8	29.3	4167	22	AAK68040	Human immune/haema
C 839	20.8	29.3	4167	22	AAK69382	Human digestive sy
C 840	20.8	29.3	4361	22	ABAI19834	Human nervous syst
C 841	20.8	29.3	4445	22	AAI26749	Human breast cance
C 842	20.8	29.3	4454	18	AAAT66462	Plasmid pCRM1.8 co
C 843	20.8	29.3	4708	23	ABLI17626	Drosophila melanog
C 844	20.8	29.3	4808	15	AAO79375	Human N-methyl-D-a
C 845	20.8	29.3	4808	21	AAV82892	Human N-methyl-D-a
C 846	20.8	29.3	4808	21	AA505015	Human N-methyl-D-a
C 847	20.8	29.3	4808	21	AA238706	Human NMDAR2a subu
C 848	20.8	29.3	4808	22	AB129172	Human NMDAR2a enco
C 849	20.8	29.3	5352	22	AAK52403	Human polynucleoti
C 850	20.8	29.3	5948	22	AA506044	Angiotensin conver
C 851	20.8	29.3	6114	21	AAAS90436	Human GAMP cDNA.
C 852	20.8	29.3	6125	22	AAH72745	Human cervical can
C 853	20.8	29.3	6242	21	AAAS99495	Human cDNA encodin
C 854	20.8	29.3	7917	23	ABLI18470	Drosophila melanog
C 855	20.8	29.3	8601	24	AB199391	Mouse ischaemic co
C 856	20.8	29.3	9402	14	AAO41345	Human hepatitis C
C 857	20.8	29.3	9407	23	AA559606	Proionibacterium
C 858	20.8	29.3	11132	22	AAK72302	Human immune/haema
C 859	20.8	29.3	11132	22	AAK72570	Human immune/haema
C 860	20.8	29.3	11200	23	ABLI1695	Drosophila melanog
C 861	20.8	29.3	11293	23	ABAI17918	Human nervous syst
C 862	20.8	29.3	13367	20	AAAX20554	Polynucleotide seq
C 863	20.8	29.3	14925	22	AAI03282	Human reproductive
C 864	20.8	29.3	14925	22	AAI04552	Human reproductive
C 865	20.8	29.3	17026	22	AAK70372	Human immune/haema
C 866	20.8	29.3	21747	22	AAK76413	Human immune/haema
C 867	20.8	29.3	21936	22	ABAI15865	Human nervous syst
C 868	20.8	29.3	21936	22	AAI06119	Human reproductive
C 869	20.8	29.3	21936	22	AAI06758	Human reproductive
C 870	20.8	29.3	21936	22	AAI62664	Human breast or ov
C 871	20.8	29.3	22107	22	ABAI17921	Human nervous syst
C 872	20.8	29.3	22107	22	AAK79542	Human immune/haema
C 873	20.8	29.3	22109	22	ABAI79543	Human nervous syst
C 874	20.8	29.3	22111	22	ABAI7919	Human immune/haema
C 875	20.8	29.3	22111	22	AAK79540	Human nervous syst
C 876	20.8	29.3	23587	22	AAI07100	Human immune/haema
C 877	20.8	29.3	24028	22	AAI05519	Human reproductive
C 878	20.8	29.3	31659	23	ABAI1694	Drosophila melanog
C 879	20.8	29.3	31813	22	ABAO8137	Human ovarian and
C 880	20.8	29.3	31813	22	AAI06997	Human reproductive
C 881	20.8	29.3	32134	22	ABAI5354	Human nervous syst
C 882	20.8	29.3	32134	22	ABAI5813	Human nervous syst
C 883	20.8	29.3	32134	22	AAI04075	Human reproductive
C 884	20.8	29.3	32134	22	AAI04075	Human reproductive
C 885	20.8	29.3	32191	22	AAI99472	Human excretory re
C 886	20.8	29.3	32191	22	AAI64117	Human bladder rela
C 887	20.8	29.3	32249	22	ABAI1755	Human nervous syst
C 888	20.8	29.3	44840	22	AAK71803	Human immune/haema
C 889	20.8	29.3	75384	22	AAK85590	Human immune/haema
C 890	20.8	29.3	349980	22	AAK85531	C glutamincum codin
C 891	20.6	29.0	182	16	AAAT24875	Human gene signatu
C 892	20.6	29.0	230	21	AAAC02258	Human secreted pro
C 893	20.6	29.0	234	22	AAI26060	Human breast cance
C 894	20.6	29.0	293	22	AAI16858	Human breast cance
C 895	20.6	29.0	493	22	AAH07332	Human cDNA clone (
C 896	20.6	29.0	519	23	AA567274	DNA encoding novel
C 897	20.6	29.0	530	22	AAI19554	Human breast cance
C 898	20.6	29.0	559	21	AAAC67954	Human breast tumou
C 899	20.6	29.0	666	22	AAH48375	Hydrogenase 9 cDNA
C 900	20.6	29.0	714	22	AAH04721	Human cDNA clone (
C 901	20.6	29.0	738	20	AAK86968	PIA acetateetyl-Co
C 902	20.6	29.0	742	22	AAI195708	Human neuroblastom
C 903	20.6	29.0	810	22	AAH01365	Serratia marcescen
C 904	20.6	29.0	840	22	AAH08571	Human cDNA clone (
C 905	20.6	29.0	925	23	AA564421	DNA encoding novel
C 906	20.6	29.0	930	23	AA564422	DNA encoding novel
C 907	20.6	29.0	972	23	ABLO5207	Drosophila melanog
C 908	20.6	29.0	981	23	AA536352	Saitmonella typhi D
C 909	20.6	29.0	991	23	ABLO4827	Human polynucleoti
C 910	20.6	29.0	1048	22	AAI58070	Human polynucleoti
C 911	20.6	29.0	1052	22	AAI59856	Human polynucleoti
C 912	20.6	29.0	1161	24	AAAD21926	M. rosaria PMR2 pl
C 913	20.6	29.0	1172	23	ABLI2997	Drosophila melanog
C 914	20.6	29.0	1289	16	AAQ99001	Bovine herpes viru
C 915	20.6	29.0	1332	23	AA579247	DNA encoding novel
C 916	20.6	29.0	1332	23	AA585618	DNA encoding novel
C 917	20.6	29.0	1332	23	AA589467	DNA encoding novel
C 918	20.6	29.0	1379	21	AAAC77752	Human cancer assoc
C 919	20.6	29.0	1400	21	AAAC62024	Nucleotide sequenc
C 920	20.6	29.0	1401	21	AACT77259	Human ORFX ORF2814
C 921	20.6	29.0	1424	22	AAH15200	Human cDNA sequenc
C 922	20.6	29.0	1500	22	AAAD05515	Human secreted pro
C 923	20.6	29.0	1602	22	AAH18715	Human cDNA sequenc
C 924	20.6	29.0	1736	17	AAAT37149	5' end of chicken
C 925	20.6	29.0	1791	23	ABLI2413	Drosophila melanog
C 926	20.6	29.0	1821	16	AAQ99366	S. lividans protea
C 927	20.6	29.0	1821	20	AAV84068	Clone p5-6 encodin
C 928	20.6	29.0	1821	21	AAAC61406	cDNA encoding a su
C 929	20.6	29.0	1823	22	AAK51475	Human polynucleoti
C 930	20.6	29.0	1827	22	AAAF61092	P. putida KT2440-a
C 931	20.6	29.0	1852	22	AAH16861	Human cDNA sequenc
C 932	20.6	29.0	1899	24	AAI67923	Human LGR6 polyep
C 933	20.6	29.0	1905	23	ABLI2412	Drosophila melanog
C 934	20.6	29.0	1926	23	AAV82522	Sphingomonas capsu
C 935	20.6	29.0	2066	23	AA579668	DNA encoding novel
C 936	20.6	29.0	2087	22	AAAF58866	Rat Glutyl coding
C 937	20.6	29.0	2122	23	AA584647	DNA encoding novel
C 938	20.6	29.0	2131	22	AAAD05492	Human secreted pro
C 939	20.6	29.0	2455	22	AAH16124	Human cDNA sequenc
C 940	20.6	29.0	2485	22	AAH14775	Human cDNA sequenc
C 941	20.6	29.0	2486	24	AAI67922	Human LGR6 polyep
C 942	20.6	29.0	2488	22	AAH17665	Human cDNA sequenc
C 943	20.6	29.0	2507	22	AAAC63398	SHEXN DNA #2. Hom
C 944	20.6	29.0	2637	22	AA526378	Human cDNA encodin
C 945	20.6	29.0	2681	23	AA558429	Thermophilus therm
C 946	20.6	29.0	2681	23	ABLO5206	Drosophila melanog
C 947	20.6	29.0	2695	23	ABLI23195	Drosophila melanog
C 948	20.6	29.0	2727	23	AA554113	Pseudomonas aerugi
C 949	20.6	29.0	2742	19	AAV23481	Pseudomonas Orfx s
C 950	20.6	29.0	2742	21	AAAI33898	Pseudomonas alcali
C 951	20.6	29.0	2742	24	AAAD22875	Pseudomonas alcali
C 952	20.6	29.0	2838	22	AAAF61007	P. putida KT2440-a
C 953	20.6	29.0	2856	23	AA556118	S. salmonella typhi D
C 954	20.6	29.0	2991	23	ABLO4826	Drosophila melanog
C 955	20.6	29.0	3000	20	AAAX84399	S. capsulata fROI2
C 956	20.6	29.0	3003	19	AAV19375	Hereditary multipl
C 957	20.6	29.0	3013	19	AAV01451	Plasmid pANT195 in
C 958	20.6	29.0	3022	23	ABLI3806	Drosophila melanog

959	20.6	29.0	3045	23	ABL21316	Drosophila melanog
960	20.6	29.0	3175	20	AAZ08224	Human Ext-2 cDNA.
961	20.6	29.0	3179	22	AAH33311	Human colon cancer
962	20.6	29.0	3311	18	AAT70377	Cytoshesin 1. Homo
963	20.6	29.0	3543	23	ABL16717	Drosophila melanog
964	20.6	29.0	3572	19	AAV67162	Drosophila kinesin
965	20.6	29.0	3610	20	ABL12996	Drosophila melanog
966	20.6	29.0	3691	23	AAV59404	Human matrix-type
967	20.6	29.0	3713	23	ABL10425	Drosophila melanog
968	20.6	29.0	3720	23	ABL13337	Drosophila melanog
969	20.6	29.0	3783	13	AB106641	Drosophila melanog
970	20.6	29.0	3789	13	AAQ30183	Bovine brain clone
971	20.6	29.0	3798	19	AAV06533	Mouse SCAT cDNA en
972	20.6	29.0	4057	23	ABL19624	Drosophila melanog
973	20.6	29.0	4418	22	AAK77953	Human immune/haema
974	20.6	29.0	4431	22	AAK77955	Human immune/haema
975	20.6	29.0	4456	22	ABL16125	Drosophila melanog
976	20.6	29.0	4614	23	ABL14340	Drosophila melanog
977	20.6	29.0	4636	21	AAV65530	Porcine BAC-PIGF2-
978	20.6	29.0	4848	24	AAZ22684	Streptomyces fradi
979	20.6	29.0	4936	22	AAZ07030	Alcaligenes latus
980	20.6	29.0	5870	22	AAZ07069	Human reproductive
981	20.6	29.0	5870	22	AAZ07069	Human immune/haema
982	20.6	29.0	6104	21	AAK77046	Human immune/haema
983	20.6	29.0	6104	21	AAK77046	Human immune/haema
984	20.6	29.0	6181	22	AAK77952	Human immune/haema
985	20.6	29.0	6192	23	ABL19622	Drosophila melanog
986	20.6	29.0	6195	22	AAK77956	Human immune/haema
987	20.6	29.0	6228	23	ABL10424	Drosophila melanog
988	20.6	29.0	6228	23	ABL06640	Drosophila melanog
989	20.6	29.0	6313	23	ABL23194	Drosophila melanog
990	20.6	29.0	6436	20	AAV66965	DNA containing PHA
991	20.6	29.0	6640	23	ABL16124	Drosophila melanog
992	20.6	29.0	6854	19	AAT76903	S. glaucosens pst
993	20.6	29.0	7014	23	ABL13336	Drosophila melanog
994	20.6	29.0	7078	22	ABL03681	Drosophila melanog
995	20.6	29.0	7120	22	AB14810	Human nervous syst
996	20.6	29.0	9320	22	AAH45588	Human encoding hydro
997	20.6	29.0	9390	19	AAT76929	GT230 genomic RNA
998	20.6	29.0	9390	19	AAT76931	GT230 gene cDNA se
999	20.6	29.0	11188	24	AAZ21912	Micromonospora ros
c1000	20.6	29.0	12468	22	AAK67330	Human Immune/haema

## ALIGNMENTS

RESULT 1

AAQ89226 standard; cDNA; 1610 BP.

AAQ89226;

20-OCT-1995 (first entry)

Human mu opioid receptor cDNA.

Mu opioid receptor; MOR; gene therapy; diagnostic; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 239..1441

FT /\*tag= a

XX MO9507983-A.

XX 23-MAR-1995.

XX 13-SEP-1994; 94MO-US10358.

XX 13-SEP-1993; 93US-0120601.

PA (INDV ) UNIV INDIANA FOUND.

XX Yu L;

XX WPI: 1995-131351/17.

DR P-PSDB; AAR71966.

XX New nucleic acid encoding new human mu opioid receptor - and

PT related vectors, transformed cells, antibodies etc., useful in

PT diagnosis, treatment and drug screening.

PS Claim 5; Page 208-210; 266pp; English.

XX A cDNA library constructed from human caudate nucleus mRNA was

CC screened with rat mu opioid receptor cDNA under conditions of

CC low stringency. One positive clone included the sequence given in

CC AAQ89226, encoding a mu opioid receptor MOR (AAR71964). The cDNA

CC is used for prodn. of recombinant MOR, in gene therapy, etc.

XX

SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other;

Query Match 100.0%; Score 71; DB 16; Length 1610;

Best Local Similarity 100.0%; Pred. No. 1, Le-13;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCTGTCCGACCCATGCGGTCCGACCGACCGACCTGGCGGAGACAGCCTGT 60

DB 354 GCACCTGTCCGACCCATGCGGTCCGACCGACCGACCGACCTGGCGGAGAGACAGCCTGT 413

QY 61 GCCCTCGACC 71

DB 414 GCCCTCGACC 424

RESULT 2

AAA59503 standard; cDNA; 1610 BP.

AAA59503;

14-NOV-2000 (first entry)

cDNA encoding a human mu opioid receptor polypeptide.

mu opioid receptor; transcription regulatory polypeptide;

opioid receptor-like polypeptide; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 239..1441

FT /\*tag= a

FT /product= "mu opioid receptor"

XX US6103492-A.

XX 15-AUG-2000.

XX 07-JUL-1997; 97US-0889108.

XX 13-SEP-1994; 94US-0305518.

XX 08-MAR-1993; 93US-0056886.

XX 13-SEP-1993; 93US-0120601.

PA (INDV ) UNIV INDIANA.

XX Yu L;

XX WPI: 2000-542550/49.

XX P-PSDB; AAB07866.

XX Novel nucleic acids encoding mu opioid receptor for expressing large

PT quantities opioid receptors which are useful for screening and

PT		evaluating subtype-selective drugs and as probes or primers -
XX		
PS	Claim 17; Column 99-102; 86pp; English.	
XX		
CC	The present sequence encodes a mu opioid receptor protein. The	
CC	specification also describes a transcription regulatory polypeptide	
CC	and an opioid receptor-like polypeptide. Human mu opioid receptor	
CC	polynucleotides are useful as a source of probes and primers, which	
CC	may be used as diagnostic tools to detect normal and abnormal DNA	
CC	sequences in DNA derived from patients cells. They are also used as	
CC	a means for detecting and isolating other members of the polypeptide	
CC	family and related polypeptides from a DNA library potentially	
CC	containing such sequences. The polynucleotide is used for preparing	
CC	large quantities of opioid receptor which on expression in	
CC	microorganism can be useful for evaluating subtype-selective drugs.	
XX		
SQ	Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other:	
	Query Match	100.0%; Score 71; DB 21; Length 1610;
	Best Local Similarity	100.0%; Pred. No. 1.le-13;
	Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 GCACCTGCCGACCATGCGGTCCGAACCCGCAGCAGCTGGGGGAGAGACAGCCTGT 60	
Db	354 GCAATTTTTCGACCCATGCGGTCCGAACCGCACCGACTGGGGGAGAGACAGCCTGT 413	
OY	61 GCCCTCCGACC 71	
Db	414 GCCCTCCGACC 424	
RESULT 3		
ID	ABI98013	
XX	ABI98013 standard; cDNA; 1182 BP.	
AC	ABI98013;	
XX		
DT	18-FEB-2002 (first entry)	
XX		
DE	Non-endogenous human GPCR cDNA, SEQ ID NO: 546.	
XX		
KW	Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;	
KW	constitutively activated GPCR; agonist; disease; ss.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	WO200177172-A2.	
XX		
PD	18-OCT-2001.	
XX		
PE	05-APR-2001; 2001WO-US11098.	
XX		
PR	07-APR-2000; 2000US-195747P.	
XX		
PA	(AREN-) ARENA PHARM INC.	
XX		
P1	Lehmann-Bruinsma K, Llaw CW, Lin I;	
XX		
DR	WPI: 2001-648759/74.	
DR	P-PSDB; ABB56377.	
PT	Identifying agonists of G protein-coupled receptors (GPCRs) for use in	
PT	disease treatment, comprises contacting candidate compounds with	
PT	versions of GPCRs -	
XX		
PS	Example 2; Page 347-348; 394pp; English.	
XX		
CC	The invention relates to G protein-coupled receptors (GPCRs) for which	
CC	the endogenous ligand has been identified. Non-endogenous	
CC	constitutively activated versions of known GPCRs are used in the	
CC	invention for the direct identification of candidate compounds as	
CC	receptor agonists, inverse agonists or partial agonists. Such	

Query Match	97.7%	Score 69.4	DB 23	Length 1182
Best Local Similarity	98.6%	Pred. No. 3.3e-13		
Matches 70: Conservative	0	Mismatches 1	Indels 0	Gaps 0
<p>agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence encodes a non-endogenous version of a known human GPCR.</p>				
Sequence 1182 BP: 292 A; 343 C; 241 G; 306 T; 0 other:				
Query Match	97.7%	Score 69.4	DB 23	Length 1182
Best Local Similarity	98.6%	Pred. No. 3.3e-13		
Matches 70: Conservative	0	Mismatches 1	Indels 0	Gaps 0
<p>agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence encodes a non-endogenous version of a known human GPCR.</p>				
Sequence 1182 BP: 292 A; 343 C; 241 G; 306 T; 0 other:				
Query Match	97.7%	Score 69.4	DB 23	Length 1203
Best Local Similarity	98.6%	Pred. No. 3.3e-13		
Matches 70: Conservative	0	Mismatches 1	Indels 0	Gaps 0
<p>agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence encodes a non-endogenous version of a known human GPCR.</p>				
Sequence 1203 BP: 301 A; 348 C; 245 G; 309 T; 0 other:				

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Db      116 GCAACCTGTCGACCCATGCGGTCCGACCGACCAACCTGGCGGAGAGACGCTGT 175
OY      61 GCCCTCCGACC 71
        |||||||
Db      176 GCCCTCCGACC 186

RESULT 5
AA093102
ID      AA093102 standard: cDNA: 2160 BP.
XX
AC      AA093102:
XX
OS      11-DEC-1995 (first entry)
XX
DE      Human mu opiate receptor cDNA.
XX
KW      Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
KW      drug abuse; analgesic; ds.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      213..1415
                /*tag= a
XX
PD      WO9520667-A1.
XX
XX      03-AUG-1995.
XX
PF      30-JAN-1995; 95WO-US01144.
XX
PR      28-JAN-1994; 94US-0188275.
XX
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA      (USSH ) US SEC DEPT HEALTH.
XX
PI      Johnson PS, Persico AM, Uhl G, Wang J;
XX
DR      MPI: 1995-275452/36.
DR      P-PSDB: AAR76780.
XX
PT      New DNA encoding human mu opiate receptor - used esp. for screening
PT      cpds. for activity as opiate agonists or antagonists
XX
PS      Claim 4: Page 24-25; 49pp; English.
XX
CC      hMOR cDNA was obtd. from a human cerebral cortical cDNA library
CC      screened with fragments of a rat mu opiate receptor. Cloned hMOR
CC      DNA can be used as probes to examine the structure and function of
CC      hMOR genes or to screen individuals for susceptibility to drug
CC      abuse. Expression in e.g. COS cells allows production of
CC      recombinant hMOR1.
XX
SQ      Sequence 2160 BP; 563 A; 566 C; 455 G; 576 T; 0 other:
Query Match      97.7%; Score 69.4; DB 16; Length 2160;
Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 GCACCTGTCCGACCCATGCGGTCCGACCGACCAACCTGGCGGAGAGACGCTGT 60
        |||||||
Db      328 GCAACCTGTCGACCCATGCGGTCCGACCGACCAACCTGGCGGAGAGACGCTGT 387
OY      61 GCCCTCCGACC 71
        |||||||
Db      388 GCCCTCCGACC 398

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```

AC      AAV61985;
XX
XX      11-JAN-1999 (first entry)
XX
DE      Human mu-opioid receptor cDNA variant 1.
XX
KW      Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW      predisposition; addiction; analgesic; anesthetic; anti-addictive;
KW      psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KW      cocaine; inherited alcoholism; human; ss.
XX
OS      Homo sapiens.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      CDS      213..2040
                /*tag= a
                /product= "mu-opioid receptor"
                /note= "b
                /*tag= b
                /note= "Site of intron 1"
                855..856
                /*tag= c
                /note= "Site of intron 2"
                1376..1377
                /*tag= d
                /note= "Site of intron 3"
                41
                /*tag= e
                /note= "Wild type G is replaced by T"
FT      mutation
FT
FT
XX      WO9833937-A2.
XX
XX      06-AUG-1998.
XX
PD      02-FEB-1998; 98WO-DE00382.
XX
PR      03-FEB-1997; 97DE-1003925.
XX
PA      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI      Hoehe M, Wendel B;
XX
DR      MPI: 1998-437487/37.
XX
PT      New genomic and cDNA sequences encoding human mu-opioid receptor -
PT      used, e.g. to predict pre-disposition to addiction and for
PT      development of analgesics, anesthetics and anti-addiction agents
XX
PS      Claim 8: Page -: 26pp; German.
XX
CC      This sequence encodes a novel human mu-opioid receptor in which a G
CC      nucleotide at position 41 of the wild-type sequence represented in
CC      AAV61984 is replaced by a T. The wild type receptor and its variants,
CC      polymorphisms and mutants are used in a method for detecting
CC      predisposition to disease, particularly addictive disease, by isolating
CC      DNA from a sample, genotyping selected positions and comparing with a
CC      reference DNA. Such sequences are used to develop analgesic,
CC      anesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC      genes and vectors, particularly for pharmaceutical development, to
CC      develop diagnostic kits for predicting risk of addiction, response to
CC      analgesics or anesthetics, or development of side effects from a drug.
CC      Particular applications are, to determine risk of addiction to opiates or
CC      cocaine, or of developing inherited alcoholism.
CC      Note: This sequence is not represented in the specification and has
CC      been constructed from the wild-type sequence represented in AAV61984 in
CC      accordance with the specification.
XX
SQ      Sequence 2162 BP; 562 A; 565 C; 457 G; 576 T; 2 other:
Query Match      97.7%; Score 69.4; DB 19; Length 2162;
Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

OY      1  GCAACCTGTCCGACCATCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60
         |||
Db      328 GCAACCTGTCCGACCATCGGTCCGAACCGACCGACCACTGGCGGAGAGACAGCCTGT 387
OY      61  GCCCTCCGACC 71
         |||
Db      388 GCCCTCCGACC 398

RESULT 7
AAV61984
ID      AAV61984 standard; cDNA; 2162 BP.
XX
AC      AAV61984;
XX
DT      11-JAN-1999 (first entry)
XX
DE      Human mu-opioid receptor cDNA.
XX
KW      Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW      predi-position; addiction; analgesic; anaesthetic; anti-addictive;
KW      psychopharmacological agent; diagnostic; side effect; drug; opiate;
KW      cocaine; inherited alcoholism; human; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      213..2040
                  /tag= a
                  /product= "mu-opioid receptor"
FT      misc_feature 502..503
                  /tag= b
                  /note= "Site of intron 1"
FT      misc_feature 855..856
                  /tag= c
                  /note= "Site of intron 2"
FT      misc_feature 1376..1377
                  /tag= d
                  /note= "Site of intron 3"
FT
XX
PN      W09833937-A2.
XX
PD      06-AUG-1998.
XX
PF      02-FEB-1998; 98WO-DE00382.
XX
PR      03-FEB-1997; 97DE-1003925.
XX
PA      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI      Hoehe M, Wendel B;
XX
DR      WPI; 1998-437487/37.
XX
PT      New genomic and cDNA sequences encoding human mu-opioid receptor -
PT      used, e.g. to predict pre-disposition to addiction and for
PT      development of analgesics, anaesthetics and anti-addiction agents
XX
PS      Claim 8; Page 14-15; 26pp; German.
XX
CC      This sequence encodes a novel human mu-opioid receptor. This sequence and
CC      its variants, polymorphisms and mutants are used in a method for
CC      detecting predi-position to disease, particularly addictive disease, by
CC      isolating DNA from a sample, genotyping selected positions and comparing
CC      with a reference DNA. Such sequences are used to develop analgesic,
CC      anaesthetic, anti-addictive and psychopharmacological agents, to construct
CC      genes and vectors, particularly for pharmaceutical development, to
CC      develop diagnostic kits for predicting risk of addiction, response to
CC      analgesics or anaesthetics, or development of side effects from a drug.
CC      Particular applications are to determine risk of addiction to opiates or
CC      cocaine, or of developing inherited alcoholism.
XX

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SQ      Sequence 2162 BP; 562 A; 565 C; 458 G; 575 T; 2 other;
Query Match      97.7%; Score 69.4; DB 19; Length 2162;
Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1  GCAACCTGTCCGACCATCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60
         |||
Db      328 GCAACCTGTCCGACCATCGGTCCGAACCGACCGACCACTGGCGGAGAGACAGCCTGT 387
OY      61  GCCCTCCGACC 71
         |||
Db      388 GCCCTCCGACC 398

RESULT 8
AAV61986
ID      AAV61986 standard; cDNA; 2162 BP.
XX
AC      AAV61986;
XX
DT      11-JAN-1999 (first entry)
XX
DE      Human mu-opioid receptor cDNA variant 2.
XX
KW      Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW      predi-position; addiction; analgesic; anaesthetic; anti-addictive;
KW      psychopharmacological agent; diagnostic; side effect; drug; opiate;
KW      cocaine; inherited alcoholism; human; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      213..2040
                  /tag= a
                  /product= "mu-opioid receptor"
FT      misc_feature 502..503
                  /tag= b
                  /note= "Site of intron 1"
FT      misc_feature 855..856
                  /tag= c
                  /note= "Site of intron 2"
FT      misc_feature 1376..1377
                  /tag= d
                  /note= "Site of intron 3"
FT      mutation 80
                  /tag= e
                  /note= "Wild type C is replaced by T"
FT
XX
PN      W09833937-A2.
XX
PD      06-AUG-1998.
XX
PF      02-FEB-1998; 98WO-DE00382.
XX
PR      03-FEB-1997; 97DE-1003925.
XX
PA      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI      Hoehe M, Wendel B;
XX
DR      WPI; 1998-437487/37.
XX
PT      New genomic and cDNA sequences encoding human mu-opioid receptor -
PT      used, e.g. to predict pre-disposition to addiction and for
PT      development of analgesics, anaesthetics and anti-addiction agents
XX
PS      Claim 8; Page -; 26pp; German.
XX
CC      This sequence encodes a novel human mu-opioid receptor in which a C
CC      nucleotide at position 80 of the wild-type sequence represented in
CC      AAV61984 is replaced by a T. The wild type receptor and its variants,

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FT      /note= "Site of intron 3"
FT      175
FT      mutation
FT      /tag= e
FT      /note= "Wild type C is replaced by A"
XX
XX
XX      WO9833937-A2.
XX
XX      06-AUG-1998.
XX
XX      02-FEB-1998; 98WO-DE00382.
XX
XX      03-FEB-1997; 97DE-1003925.
XX
XX      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX      Hoehe M, Wendel B;
XX
XX      WPI; 1998-437487/37.
XX
XX      New genomic and cDNA sequences encoding human mu-opioid receptor -
XX      used, e.g. to predict pre-disposition to addiction and for
XX      development of analgesics, anaesthetics and anti-addiction agents
XX
XX      Claim 8: Page -: 26pp; German.
XX
XX      This sequence encodes a novel human mu-opioid receptor in which a C
XX      nucleotide at position 175 of the wild-type sequence represented in
XX      AAV61984 is replaced by an A. The wild-type receptor and its variants,
XX      polymorphisms and mutants are used in a method for detecting
XX      predisposition to disease, particularly addictive disease, by isolating
XX      DNA from a sample, genotyping selected positions and comparing with a
XX      reference DNA. Such sequences are used to develop analgesic,
XX      anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
XX      genes and vectors, particularly for pharmaceutical development, to
XX      develop diagnostic kits for predicting risk of addiction, response to
XX      analgesics or anaesthetics, or development of side effects from a drug.
XX      Particular applications are to determine risk of addiction to opiates or
XX      cocaine, or of developing inherited alcoholism.
XX      Note: This sequence is not represented in the specification and has
XX      been constructed from the wild-type sequence represented in AAV61984 in
XX      accordance with the specification.
XX
XX      Sequence 2162 BP; 563 A; 564 C; 458 G; 575 T; 2 other:
XX
XX      Query Match
XX      Best Local Similarity 97.7%; Score 69.4; DB 19; Length 2162;
XX      Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0:
XX
OY      1 GCACCTGTCCGACCATCGGTCCGACCGACCGACCTGGGGGGAGAGACAGCCTGT 60
DB      328 GCAACCTGTCCGACCATCGGTCCGACCGACCGACCGACCTGGGGGGAGAGACAGCCTGT 387
OY      61 GCCCTCCGACC 71
DB      388 GCCCTCCGACC 398
XX
XX
XX      RESULT 11
XX      AAV61989
XX      ID AAV61989 standard; cDNA; 2162 BP.
XX
XX      AAV61989;
XX
XX      11-JAN-1999 (first entry)
XX
XX      Human mu-opioid receptor cDNA variant 5.
XX
XX      Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
XX      predisposition; addiction; analgesic; anaesthetic; anti-addictive;
XX      psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
XX      cocaine; inherited alcoholism; human; ss.
XX
XX      Homo sapiens.
XX

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```

OS      Synthetic.
XX
XX      Key
XX      CDS
XX      Location/Qualifiers
XX      213..2040
XX      /tag= a
XX      /product= "mu-opioid receptor"
XX      502..503
XX      /tag= b
XX      /note= "Site of intron 1"
XX      855..856
XX      /tag= c
XX      /note= "Site of intron 2"
XX      1376..1377
XX      /tag= d
XX      /note= "Site of intron 3"
XX      229
XX      /tag= e
XX      /note= "Wild type C is replaced by T"
XX
XX      WO9833937-A2.
XX
XX      06-AUG-1998.
XX
XX      02-FEB-1998; 98WO-DE00382.
XX
XX      03-FEB-1997; 97DE-1003925.
XX
XX      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX      Hoehe M, Wendel B;
XX
XX      WPI; 1998-437487/37.
XX
XX      New genomic and cDNA sequences encoding human mu-opioid receptor -
XX      used, e.g. to predict pre-disposition to addiction and for
XX      development of analgesics, anaesthetics and anti-addiction agents
XX
XX      Claim 8: Page -: 26pp; German.
XX
XX      This sequence encodes a novel human mu-opioid receptor in which a C
XX      nucleotide at position 229 of the wild-type sequence represented in
XX      AAV61984 is replaced by an T. The wild-type receptor and its variants,
XX      polymorphisms and mutants are used in a method for detecting
XX      predisposition to disease, particularly addictive disease, by isolating
XX      DNA from a sample, genotyping selected positions and comparing with a
XX      reference DNA. Such sequences are used to develop analgesic,
XX      anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
XX      genes and vectors, particularly for pharmaceutical development, to
XX      develop diagnostic kits for predicting risk of addiction, response to
XX      analgesics or anaesthetics, or development of side effects from a drug.
XX      Particular applications are to determine risk of addiction to opiates or
XX      cocaine, or of developing inherited alcoholism.
XX      Note: This sequence is not represented in the specification and has
XX      been constructed from the wild-type sequence represented in AAV61984 in
XX      accordance with the specification.
XX
XX      Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other:
XX
XX      Query Match
XX      Best Local Similarity 97.7%; Score 69.4; DB 19; Length 2162;
XX      Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0:
XX
OY      1 GCACCTGTCCGACCATCGGTCCGACCGACCGACCTGGGGGGAGAGACAGCCTGT 60
DB      328 GCAACCTGTCCGACCATCGGTCCGACCGACCGACCGACCTGGGGGGAGAGACAGCCTGT 387
OY      61 GCCCTCCGACC 71
DB      388 GCCCTCCGACC 398
XX
XX
XX      RESULT 12
XX      AAV61991
XX

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ID	AAV61991 standard; cDNA; 2162 BP.
XX	AAV61991;
AC	11-JAN-1999 (first entry)
XX	
DT	Human mu-opioid receptor cDNA variant 7.
XX	
DE	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW	predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KW	psychopharmacological agent; diagnostic; side effect; drug; opiate;
RW	cocaine; inherited alcoholism; human; ss.
XX	
OS	Homo sapiens.
XX	Synthetic.
FH	Key
XX	Location/Qualifiers
FT	213..2040
FT	/*tag= a
FT	/product= "mu-opioid receptor"
FT	502..503
FT	/*tag= b
FT	/note= "Site of Intron 1"
FT	855..856
FT	/*tag= c
FT	/note= "Site of Intron 2"
FT	1376..1377
FT	/*tag= d
FT	/note= "Site of Intron 3"
FT	666
FT	/*tag= e
FT	/note= "Wild type A is replaced by G"
XX	
PN	W09833937-A2.
XX	
PD	06-AUG-1998.
XX	
PE	02-FEB-1998; 98MO-DE00382.
XX	
PR	03-FEB-1997; 97DE-1003925.
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX	
PI	Hoelke M, Wendel B;
XX	
DR	WPI: 1998-437487/37.
XX	
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -
PT	used, e.g. to predict pre-disposition to addiction and for
PT	development of analgesics, anaesthetics and anti-addiction agents
XX	
PS	Claim 8; Page -: 26pp; German.
XX	
CC	This sequence encodes a novel human mu-opioid receptor in which an A
CC	nucleotide at position 666 of the wild-type sequence represented in
CC	AAV61994 is replaced by a G. The wild type receptor and its variants,
CC	polymorphisms and mutants are used in a method for detecting
CC	predisposition to disease, particularly addictive disease, by isolating
CC	DNA from a sample, genotyping selected positions and comparing with a
CC	reference DNA. Such sequences are used to develop analgesic,
CC	anaesthetic, anti-addictive and psychopharmacological agents, to construct
CC	genes and vectors, particularly for pharmaceutical development, to
CC	develop diagnostic kits for predicting risk of addiction, response to
CC	analgesics or anaesthetics, or development of side effects from a drug.
CC	Particular applications are to determine risk of addiction to opiates or
CC	cocaine, or of developing inherited alcoholism.
CC	Note: This sequence is not represented in the specification and has
CC	been constructed from the wild-type sequence represented in AAV61984 in
CC	accordance with the specification.
XX	
XX	
50	Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other;

Query Match 97.7%; Score 69.4; DB 19; Length 2162;

Best Local Similarity	98.6%	Pred. No. 3.5e-13;	Mismatches 1;	Indels 0;	Gaps 0;
Matches 70;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
OY	1	GCACCTGTCCGACCCATGCGTCCGAACCCGACCGACTGGCGGAGACAGACCTGT	60		
DB	328	GCACCTGTCCGACCCATGCGTCCGAACCCGACCGACTGGCGGAGAGACAGCTGT	387		
OY	61	GGCCCTCGACC	71		
DB	388	GGCCCTCGACC	398		
RESULT 13					
AAV61992					
ID	AAV61992	standard; cDNA: 2162 BP.			
XX	AAV61992;				
DT	11-JAN-1999	(first entry)			
XX					
DE	Human mu-opioid receptor cDNA variant 8.				
XX					
KW	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease; predisposition; addiction; analgesic; anaesthetic; anti-addictive; psychopharmaceutical agent; diagnostic; side effect; drug; opiate; cocaine; inherited alcoholism; human; ss.				
XX					
OS	Homo sapiens.				
OS	Synthetic.				
XX					
PH	Key	Location/Qualifiers			
FT	CDS	213..2040			
FT		/*tag= a			
FT		/product= "mu-opioid receptor"			
FT		502..503			
FT		/*tag= b			
FT		/note= "Site of intron 1"			
FT		855..856			
FT		/*tag= C			
FT		/note= "Site of intron 2"			
FT		1376..1377			
FT		/*tag= d			
FT		/note= "Site of intron 3"			
FT		1006			
FT		/*tag= e			
FT		/note= "Wild type G is replaced by A"			
XX					
PN	W09833937-A2.				
XX					
PN	06-AUG-1998.				
XX					
PF	02-FEB-1998;	98WO-DE00382.			
XX					
PR	03-FEB-1997;	97DE-1003925.			
XX					
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.				
XX					
PI	Hoehe M, Wendel B;				
XX					
DR	WPI: 1998-437487/37.				
XX					
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -				
PT	used, e.g. to predict pre-disposition to addiction and for				
PT	development of analgesics, anaesthetics and anti-addiction agents				
XX					
PS	Claim 8; Page -; 26pp; German.				
XX					
CC	This sequence encodes a novel human mu-opioid receptor in which a G				
CC	nucleotide at position 1006 of the wild-type sequence represented in				
CC	AAV61984 is replaced by an A. The wild type receptor and its variants,				
CC	polymorphisms and mutants are used in a method for detecting				
CC	predisposition to disease, particularly addictive disease, by isolating				
CC	DNA from a sample, genotyping selected positions and comparing with a				



CC	reference DNA. Such sequences are used to develop analgesic,
CC	anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC	genes and vectors, particularly for pharmaceutical development, to
CC	develop diagnostic kits for predicting risk of addiction, response to
CC	analgesics or anaesthetics, or development of side effects from a drug.
CC	Particular applications are to determine risk of addiction to opiates or
CC	cocaine, or of developing inherited alcoholism.
CC	Note: This sequence is not represented in the specification and has
CC	been constructed from the wild-type sequence represented in AAV61984 in
CC	accordance with the specification.
XX	
SQ	Sequence 2162 BP: 563 A; 565 C; 457 G; 575 T; 2 other;
XX	
Query Match	97.7%; Score 69.4; DB 19; Length 2162;
Best Local Similarity	98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative	0; Mismatches 1; Indels 0; Gaps 0.
OY	1 GCACCTGTCCACCCATGCGGTCCGAACCGCAGCCGCTGGCGGAGAGACAGCCTCT 60
Db	328 GCAACTGTGCGACCCATGCGGTCCGAACCGCAGCCACTGTGGCGGAGAGACAGCCTCT 387
OY	61 GCCCTCCGACG 71
Db	388 GCCCTCCGACG 398
RESULT 14	
AAV61993	
ID	AAV61993 standard; cDNA: 2162 BP.
XX	
AAV61993:	
DT	11-JAN-1999 (first entry)
XX	
DE	Human mu-opioid receptor cDNA variant 9.
XX	
KW	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW	predisposition; addition; analgesic; anaesthetic; anti-addictive;
KW	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KW	cocaine; inherited alcoholism; human; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	213..2040
FT	/tag= a
FT	/product= "mu-opioid receptor"
FT	502..503
FT	/tag= b
FT	/note= "Site of intron 1"
FT	855..856
FT	/tag= c
FT	/note= "Site of intron 2"
FT	1376..1377
FT	/tag= d
FT	/note= "Site of intron 3"
FT	1014
FT	/tag= e
FT	/note= "Wild type T is replaced by C"
XX	
PN	W098633937-A2.
XX	
PD	06-AUG-1998.
XX	
PE	02-FEB-1998; 98WO-DE00382.
XX	
PR	03-FEB-1997; 97DE-1003925.
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX	
P1	Hoehle M, Wendel B;
XX	

DR	WPL: 1998-437487/37.				
XX					
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -				
PT	used, e.g. to predict pre-disposition to addiction and for				
PT	development of analgesics, anaesthetics and anti-addiction agents				
XX					
PS	Claim 8; Page -: 26pp; German.				
XX					
CC	This sequence encodes a novel human mu-opioid receptor in which a T				
CC	nucleotide at position 1014 of the wild-type sequence represented in				
CC	AAV61994 is replaced by a C. The wild type receptor and its variants,				
CC	polymorphisms and mutants are used in a method for detecting				
CC	predisposition to disease, particularly addictive disease, by isolating				
CC	DNA from a sample, genotyping selected positions and comparing with a				
CC	reference DNA. Such sequences are used to develop analgesic,				
CC	anaesthetic, anti-addictive and psychopharmaceutical agents, to construct				
CC	genes and vectors, particularly for pharmaceutical development, to				
CC	develop diagnostic kits for predicting risk of addiction, response to				
CC	analgesics or anaesthetics, or development of side effects from a drug.				
CC	Particular applications are to determine risk of addiction to opiates or				
CC	cocaine, or of developing inherited alcoholism.				
CC	NOTE: This sequence is not represented in the specification and has				
CC	been constructed from the wild-type sequence represented in AAV61994 in				
CC	accordance with the specification.				
XX					
SO	Sequence 2162 BP; 562 A; 566 C; 458 G; 574 T; 2 other:				
Query Match	97.7%	Score 69.4;	DB 19;	Length 2162;	
Best Local Similarity	98.6%;	Pred. No.3.5e-13;			
Matches	70; Conservative	0; Mismatches	1; Indels	0; Gaps	
0;					
QY	1 GCACCTGTCCACCCATCGGTCCGAACCGCACCAGCCTGGCGGAGAGACAGCCTGT 60				
Db	328 GCAACCTGTCCGACCCATCGGTCCGAACCGCACCAGCCTGGCGGAGAGAGACAGCCTGT 387				
QY	61 GCCCTCCGAC 71				
Db	388 GCCCTCCGAC 398				
RESULT 15					
AAV61994	ID AAV61994 standard; cDNA; 2162 BP.				
XX					
AC	AAV61994;				
XX					
DT	11-JAN-1999 (first entry)				
XX					
DE	Human mu-opioid receptor cDNA variant 10.				
XX					
KW	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;				
KW	predisposition; addiction; analgesic; anaesthetic; anti-addictive;				
KW	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;				
XX	cocaine; inherited alcoholism; human; ss.				
XX					
OS	Homo sapiens.				
OS	Synthetic.				
XX					
FH	Key				
FT	CDS				
FT	Location/Qualifiers				
FT	213..2040				
FT	/*tag= a				
FT	/product= "mu-opioid receptor"				
FT	502..503				
FT	/*tag= b				
FT	/note= "Site of Intron 1"				
FT	855..856				
FT	/*tag= c				
FT	/note= "Site of Intron 2"				
FT	1376..1377				
FT	/*tag= d				
FT	/note= "Site of Intron 3"				
FT	1154				
FT	/*tag= e				

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FT XX /note= "Wild type G is replaced by A"
PN MO9833937-A2.
XX 06-AUG-1998.
PD 06-AUG-1998.
XX 02-FEB-1998; 98WO-DE00382.
XX 03-FEB-1997; 97DE-1003925.
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI Hoehe M, Wendel B;
XX WPI; 1998-437487/37.
DR
XX
PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
XX Claim 8; Page -: 26pp; German.
PS
XX This sequence encodes a novel human mu-opioid receptor in which a G
CC nucleotide at position 1154 of the wild-type sequence represented in
CC AAV61984 is replaced by an A. The wild-type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic,
CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anaesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in
CC accordance with the specification.
XX
XX Sequence 2162 BP; 563 A; 565 C; 457 G; 575 T; 2 other;
SQ
XX
XX Query Match 97.7%; Score 69.4; DB 19; Length 2162;
XX Best Local Similarity 98.6%; Pred. No. 3.5e-13;
XX Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGCAGCTGGCGGAGAGACAGCCTGT 60
DB 328 GCAACCTGTCCGACCCATGCGGTCCGAACCGCAGCCTGGCGGAGAGACAGCCTGT 387
XX
XX 61 GCCCTCGGACC 71
DB 388 GCCCTCGGACC 398
XX
XX RESULT 16
XX AAV61995
XX ID AAV61995 standard; cDNA; 2162 BP.
XX
XX AAV61995;
XX
XX 11-JAN-1999 (first entry)
XX
XX Human mu-opioid receptor cDNA variant 11.
XX
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
XX predisposition; addiction; analgesic; anaesthetic; anti-addictive;
XX psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
XX cocaine; inherited alcoholism; human; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX key Location/Qualifiers
FH

```

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FT XX CDS 213..2040
FT FT /tag= a
FT FT /product= "mu-opioid receptor"
FT FT misc_feature 502..503
FT FT /tag= b
FT FT /note= "Site of intron 1"
FT FT misc_feature 855..856
FT FT /tag= c
FT FT /note= "Site of intron 2"
FT FT misc_feature 1376..1377
FT FT /tag= d
FT FT /note= "Site of intron 3"
FT FT mutation 1613
FT FT /tag= e
FT FT /note= "Wild type G is replaced by C"
XX
XX
XX MO9833937-A2.
XX
XX 06-AUG-1998.
XX
XX 02-FEB-1998; 98WO-DE00382.
XX
XX 03-FEB-1997; 97DE-1003925.
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX Hoehe M, Wendel B;
XX WPI; 1998-437487/37.
XX
XX
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
XX used, e.g. to predict pre-disposition to addiction and for
XX development of analgesics, anaesthetics and anti-addiction agents
XX
XX Claim 8; Page -: 26pp; German.
PS
XX
XX This sequence encodes a novel human mu-opioid receptor in which a G
CC nucleotide at position 1613 of the wild-type sequence represented in
CC AAV61984 is replaced by a C. The wild-type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic,
CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anaesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in
CC accordance with the specification.
XX
XX Sequence 2162 BP; 562 A; 566 C; 457 G; 575 T; 2 other;
SQ
XX
XX Query Match 97.7%; Score 69.4; DB 19; Length 2162;
XX Best Local Similarity 98.6%; Pred. No. 3.5e-13;
XX Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGCAGCCTGGCGGAGAGACAGCCTGT 60
DB 328 GCAACCTGTCCGACCCATGCGGTCCGAACCGCAGCCTGGCGGAGAGACAGCCTGT 387
XX
XX 61 GCCCTCGGACC 71
DB 388 GCCCTCGGACC 398
XX
XX RESULT 17
XX AAZ88470
XX ID AAZ88470 standard; DNA; 2162 BP.
XX
XX AAZ88470;
XX

```

XX 11-MAY-2000 (first entry)  
 DT Human mu opioid receptor gene.  
 DE  
 XX  
 XX Human; mu opioid receptor; hMOR1; diagnosis; addiction; constipation;  
 KW diarrhoea; decreased immune response; stress; gastrointestinal motility;  
 KW immune response; hypothalamus pituitary adrenal axis; gonadal axis;  
 KW pain; opioid; cocaine; nicotine; barbiturate; sedative hypnotic;  
 KW anxiolytic; alcohol; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200003024-A2.  
 PN 20-JAN-2000.  
 XX  
 XX 10-JUL-1999; 99WO-US15707.  
 PF  
 XX 10-JUL-1998; 98US-0113426.  
 PR 09-JUL-1999; 99US-0113426.  
 XX  
 PA (UYRQ ) UNIV ROCKEFELLER.  
 PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.  
 XX  
 PI Kreek MJ, LaForge KS, Yu L, Tischfield JA;  
 DR WPI: 2000-160930/14.  
 DR P-PSDB: AAV79945.  
 PT New human opioid mu receptor gene variant for determining  
 PT susceptibility of a subject to addictive disorder, pain -  
 XX  
 XX Claim 1; Page -: 134pp: English.  
 PS  
 XX The present invention describes an isolated variant (V) of the human  
 CC mu opioid receptor (hMOR1) gene with at least two variations A118G,  
 CC C17T, G24A, G779A or G942A of the sequence of Genbank accession number  
 CC L25119. Determination of increased or decreased susceptibility in a  
 CC subject to at least one addictive disorder like opioid, cocaine,  
 CC nicotine, barbiturate or sedative hypnotic, anxiolytic, alcohol  
 CC addiction or addiction to others psychostimulants and to pain is done  
 CC by determining the presence of (V) with variation A118G or C17T  
 CC respectively in one and/or both alleles of (V) and it can also be done  
 CC by determining the presence of the hMOR1 protein with variation Asn40Asp  
 CC or Ala6Val respectively. Therapeutically effective amount of pain  
 CC reliever to induce analgesia or therapeutic agent to treat one additive  
 CC disorder is determined by determining the variations in the hMOR1 gene  
 CC or protein and so increased or decreased susceptibility indicates an  
 CC increased or decreased amount of pain reliever or therapeutic agent  
 CC respectively. The determination of the hMOR1 gene with variation A118G  
 CC or C17T also helps in the diagnosis of a disease or disorder like  
 CC infertility constipation, diarrhoea, decreased immune response or  
 CC decreased ability to withstand stress related to physiological function  
 CC like sexual or reproductive function, gastrointestinal motility, immune  
 CC response, or ability to withstand stress regulated by hypothalamus  
 CC pituitary adrenal axis (HPA) or gonadal axis (HPG). The present sequence  
 CC represents the hMOR1 gene.  
 CC N.B. The present sequence is not given in the present invention but  
 CC is referred to as the genbank accession number L25119.  
 CC  
 XX  
 SQ Sequence 2162 BP; 563 A; 566 C; 455 G; 576 T; 2 other;  
 Query Match 97.7%; Score 69.4; DB 21; Length 2162;  
 Best Local Similarity 98.6%; Pred. No. 3.5e-13;  
 Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 GCAACCTGCGACCGATCGGTCGACCGACCGACTGGCGGAGAGACAGCCTGT 60  
 Db 328 GCAACCTGCGACCGATCGGTCGACCGACCGACTGGCGGAGAGAGACAGCCTGT 387  
 OY 61 GCGCTCGGACC 71  
 |||||||||||

Db 388 GCGCTCGGACC 398  
 RESULT 18  
 AAV61990  
 ID AAV61990 standard; cDNA: 2162 BP.  
 XX  
 AC AAV61990;  
 XX  
 DT 11-JAN-1999 (first entry)  
 DE Human mu-opioid receptor cDNA variant 6.  
 XX  
 XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;  
 KW predisposition; addiction; analgesic; anaesthetic; anti-addictive;  
 KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;  
 KW cocaine; inherited alcoholism; human; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH CDS 213..2040  
 FT /tag= a  
 FT /product= "mu-opioid receptor"  
 FT misc\_feature 502..503  
 FT /tag= b  
 FT /note= "Site of Intron 1"  
 FT misc\_feature 855..856  
 FT /tag= c  
 FT /note= "Site of Intron 2"  
 FT misc\_feature 1376..1377  
 FT /tag= d  
 FT /note= "Site of Intron 3"  
 FT mutation 330  
 FT /tag= e  
 FT /note= "Wild type A is replaced by G"  
 XX  
 PN W09833937-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 XX 02-FEB-1998; 98WO-DE00382.  
 PF  
 XX 03-FEB-1997; 97DE-1003925.  
 PR (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
 PA Hoehe M, Wendel B;  
 PI WPI: 1998-437487/37.  
 DR  
 XX  
 XX New genomic and cDNA sequences encoding human mu-opioid receptor -  
 PT used, e.g. to predict pre-disposition to addiction and for  
 PT development of analgesics, anaesthetics and anti-addiction agents  
 XX  
 PS Claim 8; Page -: 26pp; German.  
 XX  
 CC This sequence encodes a novel human mu-opioid receptor in which an A  
 CC nucleotide at position 330 of the wild-type sequence represented in  
 CC AAV61984 is replaced by a G. The wild type receptor and its variants,  
 CC polymorphisms and mutants are used in a method for detecting  
 CC predisposition to disease, particularly addictive disease, by isolating  
 CC DNA from a sample, genotyping selected positions and comparing with a  
 CC reference DNA. Such sequences are used to develop analgesic,  
 CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct  
 CC genes and vectors, particularly for pharmaceutical development, to  
 CC develop diagnostic kits for predicting risk of addiction, response to  
 CC analgesics or anaesthetics, or development of side effects from a drug.  
 CC Particular applications are to determine risk of addiction to opiates or  
 CC cocaine, or of developing inherited alcoholism.  
 CC Note: This sequence is not represented in the specification and has  
 CC been constructed from the wild-type sequence represented in AAV61984 in

CC accordance with the specification.  
XX  
SQ Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other:  
Query Match 95.5%; Score 67.8; DB 19; Length 2162;  
Best Local Similarity 97.2%; Pred. No. 1.1e-12;  
Matches 69; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 GCAACCTGTCGACCCGATGCGTCCGAAACCGACCTGGGCGGAGAGACAGCCTGT 60  
DB 328 GGCACCTGTCCGACCCATGCGTCCGAAACCGACCAACTGGGCGGAGAGACAGCCTGT 387  
OY 61 GCCCTCCGACC 71  
DB 388 GCCCTCCGACC 398  
RESULT 19  
AAZ60728  
ID AAZ60728 standard; cDNA; 1334 BP.  
XX  
AC AAZ60728;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1D.  
XX  
KM Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;  
KM opioid-mediated ingestive response; opioid activity; analgesic;  
KM gastrointestinal motility; respiration; immune system;  
KM endocrine system; autonomic nervous system; peristalsis regulator;  
KM body weight; neuroendocrine disorder; MOR-1D; ss.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 67..1245  
FT /tag= a  
FT /product= "MOR-1D"  
FT /note= "no termination codon given"  
XX  
PN MO200004046-A2.  
XX  
PD 27-JAN-2000.  
XX  
PF 15-JUL-1999; 99WO-US15974.  
XX  
PR 16-JUL-1998; 98US-0092980.  
XX  
PA (SLOAN ) SLOAN KETTERING INST CANCER RES.  
XX  
PI Pasternak G, Pan Y;  
XX  
PI MPI: 2000-182402/16.  
XX  
DR P-PSDB; AAY68879.  
XX  
PT New splice variants of the mu-opioid receptor, useful in screening for  
PT selective analgesics and for regulating morphine analgesia or body  
PT weight -  
XX  
PS Claim 32; Fig 2B; 83pp; English.  
XX  
XX The present sequence encodes a murine mu-opioid receptor (MOR-1)  
CC splice variant MOR-1D. The specification describes 11 new exons for  
CC the MOR-1 gene, which combine to yield 15 novel splice variants of  
CC the MOR-1 gene. These splice variants are potential targets for  
CC modulating morphine analgesia and opioid-mediated ingestive responses.  
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.  
CC Such compounds are potential analgesics or more generally agents that  
CC affect gastrointestinal motility, respiration or the immune, endocrine  
CC or autonomic nervous systems, e.g. regulators of peristalsis.  
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors  
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to

CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body  
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be  
CC measured to diagnose MOR-1 related pharmacological abnormalities or  
CC neuroendocrine disorders, particularly inherited disorders. Transgenic  
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles  
CC deleted, are used to study loss or gain of function phenotypes.  
XX  
SQ Sequence 1334 BP; 320 A; 397 C; 297 G; 320 T; 0 other:  
Query Match 79.7%; Score 56.6; DB 21; Length 1334;  
Best Local Similarity 87.3%; Pred. No. 4.2e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 1 GCAACCTGTCGACCCGATGCGTCCGAAACCGACCTGGGCGGAGAGACAGCCTGT 60  
DB 176 GCAACGAGTCCGACCCATGCGTCCGAAACCGACCACTGGGCGGAGAGACAGCCTGT 235  
OY 61 GCCCTCCGACC 71  
DB 236 GCCCTCCGACC 246  
RESULT 20  
AAZ60737  
ID AAZ60737 standard; cDNA; 1346 BP.  
XX  
AC AAZ60737;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1B I.  
XX  
KM Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;  
KM opioid-mediated ingestive response; opioid activity; analgesic;  
KM gastrointestinal motility; respiration; immune system;  
KM endocrine system; autonomic nervous system; peristalsis regulator;  
KM body weight; neuroendocrine disorder; MOR-1B I; ss.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 67..1242  
FT /tag= a  
FT /product= "MOR-1B I"  
XX  
PN MO200004046-A2.  
XX  
PD 27-JAN-2000.  
XX  
PF 15-JUL-1999; 99WO-US15974.  
XX  
PR 16-JUL-1998; 98US-0092980.  
XX  
PA (SLOAN ) SLOAN KETTERING INST CANCER RES.  
XX  
PI Pasternak G, Pan Y;  
XX  
PI MPI: 2000-182402/16.  
XX  
DR P-PSDB; AAY68886.  
XX  
PT New splice variants of the mu-opioid receptor, useful in screening for  
PT selective analgesics and for regulating morphine analgesia or body  
PT weight -  
XX  
PS Claim 46; Fig 2L-W; 83pp; English.  
XX  
XX The present sequence encodes a murine mu-opioid receptor (MOR-1)  
CC splice variant MOR-1B I. The specification describes 11 new exons for  
CC the MOR-1 gene, which combine to yield 15 novel splice variants of  
CC the MOR-1 gene. These splice variants are potential targets for  
CC modulating morphine analgesia and opioid-mediated ingestive responses.  
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.  
CC Such compounds are potential analgesics or more generally agents that

CC affect gastrointestinal motility, respiration or the immune, endocrine  
CC or autonomic nervous systems, e.g. regulators of peristalsis.  
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors  
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to  
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body  
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be  
CC measured to diagnose MOR-1 related pharmacological abnormalities or  
CC neuroendocrine disorders, particularly inherited disorders. Transgenic  
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles  
CC deleted, are used to study loss or gain of function phenotypes.  
XX  
SQ Sequence 1346 BP; 338 A; 398 C; 282 G; 328 T; 0 other;  
Query Match 79.7%; Score 56.6; DB 21; Length 1346;  
Best Local Similarity 87.3%; Pred. No. 4.2e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCACCTGTCCGACCCATGCGGTCCGAACCGCAGCCTGTGGCGGAGAGACAGCCTGT 60  
DB 176 GCACCCAGTCCGACCCATGCGGTCTTAACCGCAGCGGCTTGGCGGAGACACAGCCTGT 235  
QY 61 GCCCTCCGACC 71  
DB 236 GCCCTCAGACC 246  
RESULT 21  
AAZ60736 standard; CDNA: 1365 BP.  
XX AAZ60736;  
XX 16-MAY-2000 (first entry)  
XX  
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1A.  
XX  
KW Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;  
KW opioid-mediated ingestive response; opioid activity; analgesic;  
KW gastrointestinal motility; respiration; immune system;  
KW endocrine system; autonomic nervous system; peristalsis regulator;  
KW body weight; neuroendocrine disorder; MOR-1A; ss.  
XX  
XX Mus sp.  
XX  
XX Key Location/Qualifiers  
XX FT CDS 67..1239  
XX FT /\*tag= a  
XX FT /product= "MOR-1A"  
XX  
XX MO200004046-A2.  
XX  
XX PD 27-JAN-2000.  
XX  
XX PF 15-JUL-1999; 99WO-US15974.  
XX  
XX PR 16-JUL-1998; 98US-0092980.  
XX  
XX (SLOC ) SLOAN KETTERING INST CANCER RES.  
XX  
XX Pasternak G, Pan Y;  
XX  
XX WPI: 2000-182402/16.  
XX P-PSDB: AAY68885.  
XX  
XX New splice variants of the mu-opioid receptor, useful in screening for  
XX selective analgesics and for regulating morphine analgesia or body  
XX weight -  
XX  
XX Claim 44; Fig 2J; 83pp; English.  
XX  
XX The present sequence encodes a murine mu-opioid receptor (MOR-1)  
XX splice variant MOR-1A. The specification describes 11 new exons of  
XX the MOR-1 gene, which combine to yield 15 novel splice variants of

CC the MOR-1 gene. These splice variants are potential targets for  
CC modulating morphine analgesia and opioid-mediated ingestive responses.  
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.  
CC Such compounds are potential analgesics or more generally agents that  
CC affect gastrointestinal motility, respiration or the immune, endocrine  
CC or autonomic nervous systems, e.g. regulators of peristalsis.  
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors  
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to  
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body  
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be  
CC measured to diagnose MOR-1 related pharmacological abnormalities or  
CC neuroendocrine disorders, particularly inherited disorders. Transgenic  
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles  
CC deleted, are used to study loss or gain of function phenotypes.  
XX  
SQ Sequence 1365 BP; 341 A; 399 C; 290 G; 335 T; 0 other;  
Query Match 79.7%; Score 56.6; DB 21; Length 1365;  
Best Local Similarity 87.3%; Pred. No. 4.2e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCACCTGTCCGACCCATGCGGTCCGAACCGCAGCCTGTGGCGGAGAGACAGCCTGT 60  
DB 176 GCACCCAGTCCGACCCATGCGGTCTTAACCGCAGCGGCTTGGCGGAGACACAGCCTGT 235  
QY 61 GCCCTCCGACC 71  
DB 236 GCCCTCAGACC 246  
RESULT 22  
AAZ60726 standard; CDNA: 1423 BP.  
XX AAZ60726;  
XX 16-MAY-2000 (first entry)  
XX  
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1C.  
XX  
XX  
KW Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;  
KW opioid-mediated ingestive response; opioid activity; analgesic;  
KW gastrointestinal motility; respiration; immune system;  
KW endocrine system; autonomic nervous system; peristalsis regulator;  
KW body weight; neuroendocrine disorder; MOR-1C; ss.  
XX  
XX Mus sp.  
XX  
XX Key Location/Qualifiers  
XX FT CDS 67..1383  
XX FT /\*tag= a  
XX FT /product= "MOR-1C"  
XX  
XX MO200004046-A2.  
XX  
XX PD 27-JAN-2000.  
XX  
XX PF 15-JUL-1999; 99WO-US15974.  
XX  
XX PR 16-JUL-1998; 98US-0092980.  
XX  
XX (SLOC ) SLOAN KETTERING INST CANCER RES.  
XX  
XX Pasternak G, Pan Y;  
XX  
XX WPI: 2000-182402/16.  
XX P-PSDB: AAY68877.  
XX  
XX New splice variants of the mu-opioid receptor, useful in screening for  
XX selective analgesics and for regulating morphine analgesia or body  
XX weight -  
XX  
XX Claim 30; Fig 2A; 83pp; English.  
XX  
XX

XX The present sequence encodes a murine mu-opioid receptor (MOR-1)  
CC splice variant MOR-1C. The specification describes 11 new exons for  
CC the MOR-1 gene, which combine to yield 15 novel splice variants of  
CC the MOR-1 gene. These splice variants are potential targets for  
CC modulating morphine analgesia and opioid-mediated ingestive responses.  
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.  
CC Such compounds are potential analgesics or more generally agents that  
CC affect gastrointestinal motility, respiration or the immune, endocrine  
CC or autonomic nervous systems, e.g. regulators of peristalsis.  
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors  
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to  
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body  
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be  
CC measured to diagnose MOR-1 related pharmacological abnormalities or  
CC neuroendocrine disorders, particularly inherited disorders. Transgenic  
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles  
CC deleted, are used to study loss or gain of function phenotypes.

XX Sequence 1423 BP; 343 A; 423 C; 317 G; 340 T; 0 other;

Query Match 79.7%; Score 56.6; DB 21; Length 1423;  
Best Local Similarity 87.3%; Pred. No. 4.2e-09;

Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCCGACCCATGCGGTCCGACCGACCTGGCGGGAGAGACAGCCTGT 60

DB 176 GCAACGAGTCCGACCCATGCGGTCTTAACCGACGGGCTTGGCGGGAGCAGCAGCCTGT 235

QY 61 GCCCTCGACC 71

DB 236 GCCCTCAGACC 246

#### RESULT 23

AAZ60729  
ID AAZ60729 standard; cDNA: 1542 BP.

AC AAZ60729;

DT 16-MAY-2000 (first entry)

XX cDNA encoding murine mu-opioid receptor splice variant MOR-1E.

DE Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;

KW opioid-mediated ingestive response; opioid activity; analgesic;

KW gastrointestinal motility; respiration; immune system;

KW endocrine system; autonomic nervous system; peristalsis regulator;

KW body weight; neuroendocrine disorder; MOR-1E; ss.

XX Mus sp.

OS Key Location/Qualifiers

FT CDS 67..1272

FT /tag= a

FT /transl\_except= (pos: 772..774, aa: Val)

FT /product= "MOR-1E"

XX MO200004046-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99WO-US15974.

XX 16-JUL-1998; 98US-0092980.

XX (SLOK ) SLOAN KETTERING INST CANCER RES.

XX Pasternak G, Pan Y;

XX WPI: 2000-182402/16.

XX DR P-PSDB; AAY68880.

PT New splice variants of the mu-opioid receptor, useful in screening for  
PT selective analgesics and for regulating morphine analgesia or body  
PT weight -

PS Claim 34; Fig 2C; 83pp; English.

XX The present sequence encodes a murine mu-opioid receptor (MOR-1)  
CC splice variant MOR-1E. The specification describes 11 new exons for  
CC the MOR-1 gene, which combine to yield 15 novel splice variants of  
CC the MOR-1 gene. These splice variants are potential targets for  
CC modulating morphine analgesia and opioid-mediated ingestive responses.  
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.  
CC Such compounds are potential analgesics or more generally agents that  
CC affect gastrointestinal motility, respiration or the immune, endocrine  
CC or autonomic nervous systems, e.g. regulators of peristalsis.  
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors  
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to  
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body  
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be  
CC measured to diagnose MOR-1 related pharmacological abnormalities or  
CC neuroendocrine disorders, particularly inherited disorders. Transgenic  
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles  
CC deleted, are used to study loss or gain of function phenotypes.

XX Sequence 1542 BP; 369 A; 453 C; 346 G; 374 T; 0 other;

Query Match 79.7%; Score 56.6; DB 21; Length 1542;  
Best Local Similarity 87.3%; Pred. No. 4.2e-09;

Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCCGACCCATGCGGTCCGACCGACCTGGCGGGAGAGACAGCCTGT 60

DB 176 GCAACGAGTCCGACCCATGCGGTCTTAACCGACGGGCTTGGCGGGAGCAGCAGCCTGT 235

QY 61 GCCCTCGACC 71

DB 236 GCCCTCAGACC 246

#### RESULT 24

AAZ60741  
ID AAZ60741 standard; cDNA: 1610 BP.

AC AAZ60741;

DT 16-MAY-2000 (first entry)

XX cDNA encoding murine mu-opioid receptor splice variant MOR-1.

DE Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;

KW opioid-mediated ingestive response; opioid activity; analgesic;

KW gastrointestinal motility; respiration; immune system;

KW endocrine system; autonomic nervous system; peristalsis regulator;

KW body weight; neuroendocrine disorder; MOR-1; ss.

XX Mus sp.

OS Key Location/Qualifiers

FT CDS 283..1479

FT /tag= a

FT /transl\_except= (pos: 916..918, aa: Gly)

FT /product= "MOR-1"

XX MO200004046-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99WO-US15974.

XX 16-JUL-1998; 98US-0092980.

XX (SLOK ) SLOAN KETTERING INST CANCER RES.

PI Pasternak G, Pan Y;  
XX  
XX WPI: 2000-182402/16.  
DR P-PSDB; AAY68889.  
XX  
PT New splice variants of the mu-opioid receptor, useful in screening for  
PT selective analgesics and for regulating morphine analgesia or body  
PT weight -  
XX  
XX Claim 29; Fig 2N; 83pp; English.  
PS  
XX The present sequence encodes a murine mu-opioid receptor (MOR-1)  
XX splice variant MOR-1. The specification describes 11 new exons for  
CC the MOR-1 gene, which combine to yield 15 novel splice variants of  
CC the MOR-1 gene. These splice variants are potential targets for  
CC modulating morphine analgesia and opioid-mediated ingestive responses.  
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.  
CC Such compounds are potential analgesics or more generally agents that  
CC affect gastrointestinal motility, respiration or the immune, endocrine  
CC or autonomic nervous systems, e.g. regulators of peristalsis.  
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors  
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to  
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body  
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be  
CC measured to diagnose MOR-1 related pharmacological abnormalities or  
CC neuroendocrine disorders, particularly inherited disorders. Transgenic  
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles  
CC deleted, are used to study loss or gain of function phenotypes.  
XX  
S0 Sequence 1610 BP; 373 A; 476 C; 368 G; 393 T; 0 other;  
  
Query Match 79.7%; Score 56.6; DB 21; Length 1610;  
Best Local Similarity 87.3%; Pred. No. 4.3e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
QY 1 GCAACCTGTCGACCATGCGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60  
DB 392 GCAACCAATCCGACCATGCGTCTTAACCGACGGGCGGAGACCAAGCCTGT 451  
QY 61 GCCCTCGACG 71  
DB 452 GCCCTCAGACG 462  
  
RESULT 25  
AA089222  
ID AA089222 standard; cDNA; 1618 BP.  
XX  
AC AA089222;  
XX  
DT 20-OCT-1995 (first entry)  
XX  
DE Rat mu opioid receptor cDNA.  
XX  
KM Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.  
XX  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 214..1410  
FT /tag= a  
XX  
XX WO9507983-A.  
XX  
XX 23-MAR-1995.  
XX  
XX 13-SEP-1994; 94WO-US10358.  
XX  
XX 13-SEP-1993; 93US-0120601.  
XX  
XX (INDV ) UNIV INDIANA FOUND.  
XX  
PI Yu L;

XX  
DR WPI: 1995-131351/17.  
DR P-PSDB; AAR71964.  
XX  
PT New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
XX  
XX Disclosure; Page 190-194; 266pp; English.  
PS  
XX A 365 bp fragment of the mouse delta opioid receptor was used to  
CC screen a rat brain cDNA library under low stringency conditions.  
CC One positive clone included the sequence given in AA089222, encoding a  
CC mu opioid receptor, MOR-1 (AAR71964). MOR-1 was stably expressed in  
CC transfected CHO cells.  
XX  
S0 Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other;  
  
Query Match 79.7%; Score 56.6; DB 16; Length 1618;  
Best Local Similarity 87.3%; Pred. No. 4.3e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
QY 1 GCAACCTGTCGACCATGCGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60  
DB 323 GCAACCAATCCGACCATGCGTCTTAACCGACGGGCGGAGACCAAGCCTGT 382  
QY 61 GCCCTCGACG 71  
DB 383 GCCCTCAGACG 393  
  
RESULT 26  
AA089223  
ID AA089223 standard; cDNA; 1618 BP.  
XX  
AC AA089223;  
XX  
DT 20-OCT-1995 (first entry)  
XX  
DE Transcription regulatory protein cDNA.  
XX  
KM Mu opioid receptor; MOR-1; gene therapy; diagnostic;  
XX transcription regulatory protein; ss.  
XX  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 339..1235  
FT /tag= a  
XX  
XX WO9507983-A.  
XX  
XX 23-MAR-1995.  
XX  
XX 13-SEP-1994; 94WO-US10358.  
XX  
XX 13-SEP-1993; 93US-0120601.  
XX  
XX (INDV ) UNIV INDIANA FOUND.  
XX  
XX Yu L;  
XX  
XX WPI: 1995-131351/17.  
XX  
XX P-PSDB; AAR71965.  
XX  
XX New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
XX  
XX Disclosure; Page 199-203; 266pp; English.  
XX  
XX A 365 bp fragment of the mouse delta opioid receptor was used to  
CC screen a rat brain cDNA library under low stringency conditions.

CC One positive clone included the sequence given in AA089222, encoding a  
 CC mu oploid receptor, MOR-1 (AAR71964). Sequence analysis revealed an  
 CC alternative reading frame (AA089223) encoding a zinc  
 CC finger-containing transcription regulatory protein (AAR71965).

XX Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other:

Query Match 79.7%; Score 56.6; DB 16; Length 1618;  
 Best Local Similarity 87.3%; Pred. No. 4.3e-09;  
 Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

YY 1 GCACCTGTCGACCCATCGGTCCGACCGACGACCTGGGCGGAGACAGCCTGT 60  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 DB 323 GCACCCAGTCCGATCGGTGTGAACCGACCGGCTGTGGGGAACGACAGCCTGT 382

YY 61 GCCCTCCGAC 71  
 ||||| |||||  
 DB 383 GCCCTCAGAC 393

## RESULT 27

AA059499  
 ID AA059499 standard; cDNA; 1618 BP.

XX AA059499;

DT 14-NOV-2000 (first entry)

XX cDNA encoding a mu oploid receptor polypeptide.

XX mu oploid receptor; transcription regulatory polypeptide;  
 KW oploid receptor-like polypeptide; ss.

OS Rattus sp.

XX Key Location/Qualifiers  
 FT CDS 214..1410  
 FT /tag= a  
 FT /product= "mu oploid receptor (AAB07864)"  
 FT /tag= b  
 FT /note= "alternative reading frame which encodes a  
 FT polypeptide (AAB07865) with a zinc finger motif"

XX US6103492-A.

XX 15-AUG-2000.

XX 07-JUL-1997; 97US-0889108.

XX 13-SEP-1994; 94US-0305518.

XX 08-MAR-1993; 93US-0056886.

XX 13-SEP-1993; 93US-0120601.

XX (INDV ) UNITV INDIANA.

XX YU L;

XX WPI: 2000-542550/49.

XX P-PSDB: AAB07864, AAB07865.

XX Novel nucleic acids encoding mu oploid receptor for expressing large  
 PT quantiles oploid receptors which are useful for screening and  
 PT evaluating subtype-selective drugs and as probes or primers -

XX Example 1: Column 89-92: 86bp; English.

XX The present sequence encodes a mu oploid receptor protein. The  
 CC specification also describes a transcription regulatory polypeptide  
 CC and an oploid receptor-like polypeptide. Human mu oploid receptor  
 CC polynucleotides are useful as a source of probes and primers, which  
 CC may be used as diagnostic tools to detect normal and abnormal DNA  
 CC sequences in DNA derived from patients cells. They are also used as

CC a means for detecting and isolating other members of the polypeptide  
 CC family and related polypeptides from a DNA library potentially  
 CC containing such sequences. The polynucleotide is used for preparing  
 CC large quantiles of oploid receptor which on expression in  
 CC microorganism can be useful for evaluating subtype-selective drugs.

XX Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other:

Query Match 79.7%; Score 56.6; DB 21; Length 1618;  
 Best Local Similarity 87.3%; Pred. No. 4.3e-09;  
 Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

YY 1 GCACCTGTCGACCCATCGGTCCGACCGACGACCTGGGCGGAGACAGCCTGT 60  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 DB 323 GCACCCAGTCCGATCGGTGTGAACCGACCGGCTGTGGGGAACGACAGCCTGT 382

YY 61 GCCCTCCGAC 71  
 ||||| |||||  
 DB 383 GCCCTCAGAC 393

## RESULT 28

AA060734  
 ID AA060734 standard; cDNA; 1729 BP.

XX AA060734;

DT 16-MAY-2000 (first entry)

XX cDNA encoding murine mu-oploid receptor splice variant MOR-1F.

XX Mu-oploid receptor; MOR-1; splice variant; morphine analgesia;  
 KW oploid-mediated ingestive response; oploid activity; analgesic;  
 KW gastrointestinal motility; respiration; immune system;  
 KW endocrine system; autonomous nervous system; peristalsis regulator;  
 KW body weight; neuroendocrine disorder; MOR-1F; ss.

XX Mus sp.

XX Key Location/Qualifiers  
 FT CDS 67..1401  
 FT /tag= a  
 FT /product= "MOR-1F"

XX WO200004046-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99WO-US15974.

XX 16-JUL-1998; 98US-0092980.

XX (SLOK ) SLOAN KETTERING INST CANCER RES.

XX Pasternak G, Pan Y;

XX WPI: 2000-182402/16.

XX P-PSDB: AAY68888.

XX New splice variants of the mu-oploid receptor, useful in screening for  
 PT selective analgesics and for regulating morphine analgesia or body  
 PT weight -

XX Claim 36; Fig 2F; 83bp; English.

XX The present sequence encodes a murine mu-oploid receptor (MOR-1)  
 CC splice variant MOR-1F. The specification describes 11 new exons for  
 CC the MOR-1 gene, which combine to yield 15 novel splice variants of  
 CC the MOR-1 gene. These splice variants are potential targets for  
 CC modulating morphine analgesia and oploid-mediated ingestive responses.  
 CC The MOR-1 polypeptide is used to screen compounds for oploid activity.  
 CC Such compounds are potential analgesics or more generally agents that  
 CC affect gastrointestinal motility, respiration or the immune, endocrine



CC or autonomous nervous systems, e.g. regulators of peristalsis.  
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors  
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to  
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body  
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be  
CC measured to diagnose MOR-1 related pharmacological abnormalities or  
CC neuroendocrine disorders, particularly inherited disorders. Transgenic  
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles  
CC deleted, are used to study loss or gain of function phenotypes.  
SQ Sequence 1729 BP; 417 A; 505 C; 395 G; 412 T; 0 other;  
Query Match 79.7%; Score 56.6; DB 21; Length 1729;  
Best Local Similarity 87.3%; Pred. No. 4.3e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCACCTGTCCGACCCATGCGTCCGAACCGCAGCCGACCTGTGT 60  
DB 176 GCACCCAGTCCGACCCATGCGTCTTAACCGCAGGCGGTGCGAGCCACAGCTGT 235  
QY 61 GCCCTCCGACC 71  
DB 236 GCCCTCAGACC 246  
RESULT 29  
AAZ60735  
ID AAZ60735 standard; cDNA; 2045 BP.  
XX  
AC AAZ60735;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1B II.  
XX  
XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;  
XX opiod-mediated ingestive response; opiod activity; analgesic;  
XX gastrointestinal motility; respiration; immune system;  
XX endocrine system; autonomous nervous system; peristalsis regulator;  
XX body weight; neuroendocrine disorder; MOR-1B II; ss.  
XX  
OS Mus sp.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 67..1296  
FT /\*tag= a  
FT /transl\_except= (pos: 601..603, aa: Gly)  
FT /product= "MOR-1B II"  
XX  
XX MO200004046-A2.  
XX  
XX  
XX 27-JAN-2000.  
XX  
XX 15-JUL-1999; 99WO-US15974.  
XX  
XX 16-JUL-1998; 98US-0092980.  
XX  
XX (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX  
XX Pasternak G, Pan Y;  
XX  
XX WPI: 2000-182402/16.  
XX  
XX P-PSDB: AAY68887.  
XX  
XX  
XX New splice variants of the mu-opioid receptor, useful in screening for  
XX selective analgesics and for regulating morphine analgesia or body  
XX weight  
XX  
XX  
XX Claim 42; Fig 2H; 83pp; English.  
XX  
XX The present sequence encodes a murine mu-opioid receptor (MOR-1)  
XX splice variant MOR-1B II. The specification describes 11 new exons for  
XX the MOR-1 gene, which combine to yield 15 novel splice variants of

CC the MOR-1 gene. These splice variants are potential targets for  
CC modulating morphine analgesia and opiod-mediated ingestive responses.  
CC The MOR-1 polypeptide is used to screen compounds for opiod activity.  
CC Such compounds are potential analgesics or more generally agents that  
CC affect gastrointestinal motility, respiration or the immune, endocrine  
CC or autonomous nervous systems, e.g. regulators of peristalsis.  
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors  
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to  
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body  
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be  
CC measured to diagnose MOR-1 related pharmacological abnormalities or  
CC neuroendocrine disorders, particularly inherited disorders. Transgenic  
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles  
CC deleted, are used to study loss or gain of function phenotypes.  
SQ Sequence 2045 BP; 521 A; 526 C; 422 G; 576 T; 0 other;  
Query Match 79.7%; Score 56.6; DB 21; Length 2045;  
Best Local Similarity 87.3%; Pred. No. 4.4e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCACCTGTCCGACCCATGCGTCCGAACCGCAGCCGACCTGTGT 60  
DB 176 GCACCCAGTCCGACCCATGCGTCTTAACCGCAGGCGGTGCGAGCCACAGCTGT 235  
QY 61 GCCCTCCGACC 71  
DB 236 GCCCTCAGACC 246  
RESULT 30  
AAF85416  
ID AAF85416 standard; cDNA to mRNA; 2135 BP.  
XX  
XX AAF85416;  
XX  
XX 23-JUL-2001 (first entry)  
XX  
XX Nucleotide sequence of a rat mu-subtype opiate receptor.  
XX  
XX  
XX mu-subtype opiod receptor; G protein; opiod; drug addiction; ss.  
XX  
XX  
XX  
OS Rattus rattus.  
XX  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 157..1227  
FT /\*tag= a  
FT /product= "mu-subtype opiate receptor"  
FT /transl\_except= "(pos: 157..159, aa: Met)"  
FT /transl\_except= "(pos: 160..162, aa: Arg)"  
FT /transl\_except= "(pos: 163..165, aa: Ser)"  
FT /transl\_except= "(pos: 166..168, aa: Glu)"  
FT /transl\_except= "(pos: 169..171, aa: Pro)"  
FT /transl\_except= "(pos: 232..234, aa: Gly)"  
XX  
XX  
XX US6225080-B1.  
XX  
XX  
XX 01-MAY-2001.  
XX  
XX 28-APR-1995; 95US-0430286.  
XX  
XX 11-JUN-1993; 93US-0075447.  
XX  
XX 23-MAR-1992; 92US-0855286.  
XX  
XX 26-FEB-1993; 93US-0026140.  
XX  
XX (UHLG/) UHL G R.  
XX (EPPL/) EPPLER C M.  
XX (WANG/) WANG J.  
XX  
XX Uhl GR, Eppler CM, Wang J;  
XX  
XX WPI: 2001-342395/36.  
XX  
XX P-PSDB: AAB68440.

XX Novel isolated DNA encoding mu-subtype opioid receptor protein which is  
PT useful for identifying other receptor subtypes, screening for mu opioid  
PT ligands and for understanding mechanisms of opioid action  
XX  
PS Claim 1; Column 17-20; 51pp; English.  
XX  
XX The present sequence encodes a rat mu-subtype opioid receptor. The  
CC polynucleotide sequence is useful for producing a mu-type opioid  
CC receptor by standard recombinant techniques. The encoded protein is  
CC useful for producing monoclonal or polyclonal anti-receptor antibodies  
CC and to identify patterns of post-translational modifications and to  
CC elucidate associated G proteins. Mu receptor polynucleotides and  
CC polypeptides are useful in identifying other receptor subtypes, in  
CC screening for new opioid ligands and for understanding mechanisms of  
CC opioid action e.g., drug addiction.  
XX  
SQ Sequence 2135 BP; 541 A; 590 C; 441 G; 563 T; 0 other;  
Query Match 79.7%; Score 56.6; DB 22; Length 2135;  
Best Local Similarity 87.3%; Pred. No. 4.4e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGACCGACTGGCGGAGAGACAGCCTGT 60  
DB 140 GCAACCGAGTCCGATCGGTCTGCTGAACCGACCGGCTTGGCGGAGAGACAGCCTGT 199  
QY 61 GCCCTCCGACC 71  
DB 200 GCCCTCAGACC 210  
RESULT 31  
AAV49252  
ID AAV49252 standard; DNA; 2229 BP.  
XX  
AC AAV49252;  
XX  
DT 28-OCT-1998 (first entry)  
XX  
DE Mouse mu opiate receptor gene.  
XX  
XX Mouse; mu opiate receptor; transgenic animal; mammal; identification;  
KW exon; nervous tissue; pain; drug addiction; transplant rejection;  
KM immunosuppressant; analgesic; morphine; side effect; ds.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 256..1452  
FT /\*tag= a  
FT /product= "mu opiate receptor"  
XX  
PN MO9802534-A2.  
XX  
PD 22-JAN-1998.  
XX  
PF 11-JUL-1997; 97MO-FR01282.  
XX  
PR 15-JUL-1996; 96FR-0008810.  
XX  
PA (CNRS ) CENT NAT RECH SCI.  
XX  
PI Dierich A, Kieffer BL, Lémur M, Matthes HMD, Simonin FH;  
XX  
DR WPI; 1998-110582/10.  
XX  
DR P-PADB; AAW4937.  
XX  
PT Transgenic animals defective in one type of opioid receptor - used  
PT to identify agents for treatment of pain, drug addiction and  
PT transplant rejection, lacking side effects of known opiate(s)  
XX  
PS Disclosure: Fig 11; 58pp; French.

XX This sequence represents the gene encoding the mouse mu opiate receptor  
CC protein. The sequence is used to generate a transgenic non-human mammal  
CC for identifying agents for treating disorders associated with opiate  
CC receptors. In the mammal, the expression of the gene encoding the opiate  
CC receptor is modified, particularly by the deletion of an exon and/or  
CC insertion of a marker gene, e.g. the neomycin resistance gene, into the  
CC sequence. Especially the expression of the gene is altered in nervous  
CC tissue. The agents are potentially useful for treating severe pain  
CC (chronic or acute), drug addiction and/or prevention or treatment of  
CC transplant rejection (as immunosuppressants). The method may isolate and  
CC identify powerful analgesics that lack morphine-like side effects.  
XX  
SQ Sequence 2229 BP; 562 A; 608 C; 489 G; 570 T; 0 other;  
Query Match 79.7%; Score 56.6; DB 19; Length 2229;  
Best Local Similarity 87.3%; Pred. No. 4.4e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGACCGACTGGCGGAGAGACAGCCTGT 60  
DB 365 GCAACCGAGTCCGATCGGTCTGCTGAACCGACCGGCTTGGCGGAGAGACAGCCTGT 424  
QY 61 GCCCTCCGACC 71  
DB 425 GCCCTCAGACC 435  
RESULT 32  
AAQ56705  
ID AAQ56705 standard; cDNA; 1981 BP.  
XX  
AC AAQ56705;  
XX  
DT 15-SEP-1994 (first entry)  
XX  
DE Partial sequence of the murine mu-receptor clone DOR-2  
DE (MOR-1, MOR-1alpha).  
XX  
XX Opioid receptor; morphine; opiate; ss.  
XX  
OS Mus musculus.  
XX  
PN WO9404552-A.  
XX  
PD 03-MAR-1994.  
XX  
PF 13-AUG-1993; 93WO-US07665.  
XX  
PR 13-AUG-1992; 92US-0929200.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;  
XX  
DR WPI; 1994-083099/10.  
XX  
PT DNA encoding opioid receptors and antibodies against this  
PT receptor - used to express and locate these receptors, and screen  
PT opds. for opioid (antagonist activity)  
XX  
PS Example; Fig 9; 74pp; English.  
XX  
XX A cDNA library prep. from mouse brain was probed using DOR-1 (see  
CC AAQ56704) as a probe. One clone was recovered and sequenced. This  
CC clone, designated DOR-2, represented a new gene. DOR-2 hybridised  
CC to a different pattern of neurons than did DOR-1 and showed greater  
CC labeling of the striatum. The identity of DOR-2 (mMOR-1) as that of  
CC a mu receptor was confirmed.  
XX  
SQ Sequence 1981 BP; 499 A; 549 C; 436 G; 496 T; 1 other;  
Query Match 75.2%; Score 53.4; DB 15; Length 1981;



```

XX AA079199;
AC 19-APR-1995 (first entry)
DE Rat mu-subtype opioid receptor cDNA.
XX Mu-subtype opioid receptor; MSOR; drug addiction; ds.
XX Rattus rattus.
OS
XX
XX Key Location/Qualifiers
XX CDS 83..1154
XX FT /*tag= a
XX FT /product= Mu-subtype_opioid_receptor
XX
XX EP612845-A.
XX
XX 31-AUG-1994.
XX
XX 09-FEB-1994; 94EP-0101968.
XX
XX 26-FEB-1993; 93US-0026140.
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Corbett MJ, Eppler CM, Shieh H, Zysk JR;
XX WPI; 1994-265963/33.
XX P-PSDB; AAR65188.
XX
XX Pure mu-type opioid receptor protein - and nucleic acid coding
XX for it
XX
XX Claim 1; Fig 11; 39pp; English.
XX
XX AAR65188 is the rat mu-subtype opioid receptor protein purified
XX from rat brain membranes, with biotinyl-b-endorphin (AAR56666)
XX as its ligand. It is encoded by the nucleotide sequence AA079199
XX which was synthesised using AA071022 and AA071023 as PCR primers.
XX AAR65188 is useful for identifying other receptor subtypes, for
XX screening new opioid ligands, and for studying mechanisms of
XX opioid action, e.g. drug addiction.
XX
XX Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T; 0 other;
SQ
XX
XX Query Match 62.8%; Score 44.6; DB 15; Length 2070;
XX Best Local Similarity 85.9%; Pred. No. 3e-05; 9; Indels 1; Gaps 1;
XX Matches 61; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
XX
XX 1 GCAACCTGTCCGACCATGGCTCCGAACCGACGACCTGGCGGAGAGACAGCCTGT 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 76 GCAACCATGGCTCCGATCGGCTGTGAACCG-ACCGGGCTTGGGAGACAGACCTGT 134
XX
XX 61 GCCCTCCGACC 71
XX ||||| |||||
XX Db 135 GCCCTCAGACC 145
XX
XX
XX RESULT 36
XX ABL33392
XX ID ABL33392 standard; DNA: 6494 BP.
XX
XX ABL33392;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human immune system associated gene SEQ ID NO: 1365.
XX
XX Human immune system disease; cytosine methylation; antiasthmatic;
XX antiarteriosclerotic; antihaemic; cytosine; noctropic;
XX neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
XX antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

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```

XX antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
XX gene; ds.
XX
XX Homo sapiens.
XX
XX WO200200928-A2.
XX
XX 03-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07537.
XX
XX 30-JUN-2000; 2000DE-1032529.
XX PR 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful
XX for diagnosis and treatment of diseases associated with abnormal
XX cytosine methylation
XX
XX Claim 1; SEQ ID NO 1365; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
XX can be used in the diagnosis and treatment of immune system disorders,
XX including eye diseases such as retinopathy, neovascular glaucoma and
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX diseases. The present sequence is a gene of the invention.
XX
XX Sequence 6494 BP; 2088 A; 81 C; 1298 G; 3027 T; 0 other;
SQ
XX
XX Query Match 52.7%; Score 37.4; DB 24; Length 6494;
XX Best Local Similarity 70.4%; Pred. No. 0.0068; 21; Indels 0; Gaps 0;
XX Matches 50; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
XX
XX 1 GCAACCTGTCCGACCATGGCTCCGAACCGACGACCTGGCGGAGAGACAGCCTGT 60
XX ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 5320 GTAATTGTTCGATTTATCGGTTCCGATTCGATTTGGCGGAGAGATGTTGT 5379
XX
XX 61 GCCCTCCGACC 71
XX ||| ||| |||
XX Db 5380 GTTTTTCGATC 5390
XX
XX
XX RESULT 37
XX AAS08693/C
XX ID AAS08693 standard; DNA: 109519 BP.
XX
XX AAS08693;
XX
XX 26-SEP-2001 (first entry)
XX
XX Micromonospora DNA encoding biosynthetic enzymes for Evernimycin.
XX
XX Evernimycin; antibiotic; bottle-neck gene; orthomycin;
XX fermentation; ds.
XX
XX Micromonospora carbonacea var. africana.
XX
XX Key Location/Qualifiers
XX CDS complement (132..1382)
XX FT /*tag= a
XX FT /product= "Evda"
XX FT complement (1389..1394)
XX RBS /*tag= b

```

FT	CDS	complement (1490..2611)	FT	RBS	/product= "EvrC"
FT		/*tag= c	FT		22736..22740
FT	RBS	/product= "EvdB"	FT	CDS	/*tag= ad
FT		complement (2618..2622)	FT		complement (24177..25223)
FT	CDS	/*tag= d	FT		/*tag= ae
FT		complement (2622..3860)	FT	RBS	/product= "EvrH"
FT		/*tag= e	FT		complement (25230..25233)
FT	RBS	/product= "EvdC"	FT		/*tag= af
FT		complement (3867..3870)	FT	CDS	25550..26626
FT		/*tag= f	FT		/*tag= ag
FT	CDS	4143..5312	FT		/product= "EvrI"
FT		/*tag= g	FT	CDS	26685..30479
FT	RBS	/product= "EvdD"	FT		/*tag= ah
FT		4134..4138	FT		/product= "EvrJ"
FT	CDS	/*tag= h	FT		26672..26676
FT		5309..6235	FT	CDS	/*tag= ai
FT		/*tag= i	FT		complement (30557..31876)
FT	CDS	/product= "EvdE"	FT		/*tag= aj
FT		6232..7275	FT	RBS	/product= "EvrK"
FT		/*tag= j	FT		complement (31885..31888)
FT	RBS	/product= "EvdF"	FT		/*tag= ak
FT		6226..6229	FT	CDS	complement (31941..32882)
FT	CDS	/*tag= k	FT		/*tag= al
FT		7272..8327	FT		/product= "EvrL"
FT		/*tag= l	FT	CDS	complement (33167..34405)
FT	CDS	/product= "EvdG"	FT		/*tag= am
FT		8342..9364	FT	RBS	/product= "EvrM"
FT		/*tag= m	FT		complement (34414..34418)
FT	RBS	/product= "EvdH"	FT	CDS	/*tag= an
FT		8333..8336	FT		complement (34449..35210)
FT	CDS	/*tag= n	FT		/*tag= ao
FT		complement (9463..10224)	FT	RBS	/product= "EvrN"
FT		/*tag= o	FT		complement (35219..35221)
FT	RBS	/product= "EvdI"	FT	CDS	/*tag= ap
FT		complement (10232..10235)	FT		complement (35294..36238)
FT	CDS	/*tag= p	FT		/*tag= aq
FT		10424..11176	FT	CDS	/product= "EvrO"
FT		/*tag= q	FT		complement (36235..36963)
FT	CDS	/product= "EvdJ"	FT		/*tag= ar
FT		12027..12455	FT	CDS	/product= "EvrP"
FT		/*tag= r	FT		complement (36998..38026)
FT		/product= "EvdK"	FT	CDS	/*tag= as
FT		/partial	FT		/product= "EvrQ"
FT	CDS	/note= "No start codon"	FT		complement (38072..38566)
FT		complement (12108..13022)	FT	CDS	/*tag= at
FT		/*tag= s	FT		/product= "EvrR"
FT	RBS	/product= "EvdL"	FT		complement (38892..40163)
FT		complement (13027..13030)	FT	CDS	/*tag= au
FT		/*tag= t	FT		/product= "EvrS"
FT	CDS	complement (14410..15363)	FT		complement (40216..40890)
FT		/*tag= u	FT		/*tag= av
FT	RBS	/product= "EvrA"	FT		/product= "EvrT"
FT		complement (15369..15373)	FT	CDS	complement (40899..40902)
FT		/*tag= v	FT		/*tag= aw
FT	CDS	complement (15380..16414)	FT		complement (40887..41576)
FT		/*tag= w	FT		/*tag= ax
FT	CDS	/product= "EvrB"	FT		/product= "EvrU"
FT		complement 16419..17873	FT	CDS	complement (41679..42707)
FT		/*tag= x	FT		/*tag= ay
FT	CDS	/product= "EvrC"	FT		/product= "EvrV"
FT		complement (17870..18934)	FT	RBS	complement (42714..42717)
FT		/*tag= y	FT		/*tag= az
FT	CDS	/product= "EvrD"	FT		complement (42810..43799)
FT		19374..20906	FT		/*tag= ba
FT		/*tag= z	FT	RBS	/product= "EvrW"
FT	CDS	/product= "EvrE"	FT		complement (43807..43811)
FT		21064..22542	FT	CDS	/*tag= bb
FT		/*tag= aa	FT		complement (43799..44866)
FT	RBS	/product= "EvrF"	FT		/*tag= bc
FT		21056..22542	FT	CDS	/product= "EvrX"
FT		/*tag= ab	FT		complement (45014..45760)
FT	CDS	22748..24172	FT		/*tag= bd
FT		/*tag= ac	FT		/product= "EvrY"

```
FT RBS complement (45767..45770)
FT CDS /*tag- be
FT CDS complement (45962..46714)
FT CDS /*tag- bf
FT RBS /product- "EVR2"
FT CDS complement (45952..45956)
FT CDS /*tag- bg
FT CDS complement (47156..49234)
FT CDS /*tag- bh
FT CDS /product- "EVSa"
FT CDS 51627..52715
FT CDS /*tag- bi
FT RBS /product- "EVSb"
FT CDS 51629..51622
FT CDS /*tag- bj
FT CDS 52889..53557
FT CDS /*tag- bk
FT CDS /product- "EVCc"
FT CDS 53554..54207
FT CDS /*tag- bl
FT CDS /product- "EVDa"
FT CDS complement (54362..55117)
FT CDS /*tag- bm
FT RBS /product- "EVDc"
FT CDS complement (55125..55128)
FT CDS /*tag- bn
FT CDS complement (55135..56094)
FT CDS /*tag- bo
FT RBS /product- "EVCc"
FT CDS complement (56100..56103)
FT CDS /*tag- bp
FT CDS complement (56184..56813)
FT CDS /*tag- bq
FT CDS /product- "EVCc2"
FT CDS 56961..58709
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Query Match 37.28; Score 26.4; DB 22; Length 109519;  
Best Local Similarity 65.0%; Pred. No. 30;  
Matches 39; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 11 CGACCCATGCGCTCGAAGCCGACGCTGGGGGAGAGACACGCTGTCCTCGAC 70  
Db 9489 CGACCTGTGCTGACGACGGAGCTGCGCGGGCGCGCTGTGAGACCGCGAC 9430

RESULT 38  
AAK93041  
ID AAK93041 standard; cDNA: 527 BP.

AC AAK93041;

DT 06-NOV-2001 (first entry)

DE Human cDNA 3'-end sequence, SEQ ID NO: 1501.

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.

PN EP1130094-A2.

PD 05-SEP-2001.

PF 07-JUL-2000; 2000EP-0114089.

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

PA (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,  
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

```
XX WPI: 2001-524255/58.
DR 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX Claim 3: SEQ ID NO 1501; 1380bp + sequence listing; English.
XX The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is the nucleotide
CC sequence of the 3'-end of a cDNA provided in the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
```

Sequence 527 BP; 112 A; 160 C; 161 G; 84 T; 10 other;

Query Match 36.18; Score 25.6; DB 22; Length 527;  
Best Local Similarity 66.1%; Pred. No. 31;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 GCACCTGTGCTGCGAAGCCGACGCTGGGGGAGAGACAGC 56  
Db 39 GCACCTGTGCTGCGAAGCCGACGCTGGGGGAGAGAGATGC 94

RESULT 39  
AAC90469/c  
ID AAC90469 standard; cDNA: 1178 BP.

AC AAC90469;

DT 12-MAR-2001 (first entry)

DE Human uncoupling protein cDNA #18.

KW Human; uncoupling protein; immunosuppressive; antiarthritic;

KW antirheumatic; antiproliferative; cardiant; vasotropic;

KW cerebroprotective; neuroprotective; antibacterial; optalmological;

KW gastrointestinal; nephrotropic; gynaecological; vulnerrary; thrombolytic;

KW gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;

KW infertility; ss.

OS Homo sapiens.

PN WO200061614-A2.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US09534.

PR 09-APR-1999; 99US-0128701.

PR 08-JUL-1999; 99US-0142821.

PR 18-AUG-1999; 99US-0149448.

PR 12-NOV-1999; 99US-0164751.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Ni J, Komatsoulis G, Rosen CA, Soppet DR;  
WPI: 2000-656322/63.  
P-PSDB; AAB50395.

Uncoupling proteins and nucleic acid sequences encoding them, useful  
for detecting, preventing and treating proliferative, neurological,  
immune system, cardiovascular and gastrointestinal disorders -

PS Claim 1; Page 315-316; 343pp; English.  
XX The present sequence is one of eighteen isolated nucleotide sequences  
CC encoding uncoupling proteins. The nucleotide sequences may be used for  
CC the detection of various disorders such as cancer, for chromosome  
CC identification, as chromosome markers and for numerous other diagnostic  
CC or research purposes. The uncoupling protein encoded by the nucleotide  
CC sequences may be used to treat disorders such as neural, immune,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders, wounds, infectious diseases,  
CC thrombosis, arthritis, and infertility.  
XX  
SQ Sequence 1178 BP; 239 A; 388 C; 329 G; 222 T; 0 other:  
XX  
Query Match 36.1%; Score 25.6; DB 21; Length 1178;  
Best Local Similarity 66.1%; Pred. No. 34;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
OY 1 GCACCTGTCCGACCCATGCGTCCGAACCGCAGCTGGCGGAGACAGC 56  
DB 1074 GCACACTGCGCTTCCAGGTGGGTGAAGCCAGCAGGAGGAGGATGTC 1019  
RESULT 40  
AA160768 standard; cDNA: 1856 BP.  
XX  
AC AA160768;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polynucleotide SEQ ID NO 4757.  
XX  
XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia; ss.  
XX  
XX Homo sapiens.  
OS  
PN WO200153312-A1.  
XX  
XX 26-JUL-2001.  
PD  
XX 26-DEC-2000; 2000WO-US34263.  
PE  
XX 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX  
XX (HSE-) HXSEQ INC.  
XX  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Mehran T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX  
XX WPI: 2001-442253/47.  
DR P-PSDB; AAM41612.  
XX  
XX Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -  
XX  
XX Claim 1; SEQ ID NO 4757; 10078pp; English.  
XX  
XX The invention relates to human nucleic acids (AA157798-AA161369) and  
CC the encoded polypeptides (AAM38642-AAM42213) with noctropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localized neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager syndrome. Other uses include the  
CC utilisation of the activities such as: immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.  
XX  
SQ Sequence 1856 BP; 370 A; 572 C; 611 G; 303 T; 0 other:  
XX  
Query Match 36.1%; Score 25.6; DB 22; Length 1856;  
Best Local Similarity 66.1%; Pred. No. 35;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
OY 1 GCACCTGTCCGACCCATGCGTCCGAACCGCAGCTGGCGGAGACAGC 56  
DB 51 GCACACTGCGCTTCCAGGTGGGTGAAGCCAGCAGGAGGAGGATGTC 106  
RESULT 41  
AAK94578/C  
ID AAK94578 standard; cDNA: 1872 BP.  
XX  
XX AAK94578;  
XX  
AC AAK94578;  
XX  
XX 06-NOV-2001 (first entry)  
DT  
XX  
DE Human full-length cDNA, SEQ ID NO: 3500.  
XX  
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
KW  
XX  
XX Homo sapiens.  
OS  
PN EP1130094-A2.  
XX  
XX 05-SEP-2001.  
PD  
XX 07-JUL-2000; 2000EP-0114089.  
PE  
XX 08-JUL-1999; 99JP-0194486.  
PR 11-JAN-2000; 2000JP-0118774.  
PR 02-MAY-2000; 2000JP-0183765.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
PI  
XX  
XX WPI: 2001-524255/58.  
DR P-PSDB; AAM93644.  
XX  
XX 830 Primers useful for synthesizing full length cDNA clones and their  
PT use in genetic manipulation -  
XX  
XX Claim 8; SEQ ID NO 3500; 1380pp + sequence listing; English.  
XX  
XX The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been  
CC isolated and nucleotide sequences of 5' - and 3'-ends of the cDNA  
CC molecules have been determined. Primers for synthesizing the full length  
CC cDNA are useful for clarifying the function of the protein encoded by  
CC the cDNA. The full length clones were obtained by construction of full  
CC length enriched cDNA libraries that were synthesised by the oligo-capping  
CC method. The primers enable the production of the full length cDNA easily  
CC without any special methods. The present sequence is a full length  
CC human cDNA of the invention.

CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in CD-ROM format directly from EPO.  
XX  
SQ Sequence 1872 BP; 294 A; 621 C; 588 G; 369 T; 0 other;

Query Match 36.1%; Score 25.6; DB 22; Length 1872;  
Best Local Similarity 66.1%; Pred. No. 35;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 GCAACCTGTCGACCCATGCGGTCCGACCGACCTGGCGGAGAGACAGC 56  
DB 1834 GCACACTGCCCCCTTCCAGGTGGGTGAAGCCAGCAGCAGGAGGAGGATGC 1779

RESULT 42  
ID AAI58982/c  
AAI58982 standard; cDNA; 2003 BP.

AC AAI58982;  
XX  
DT 22-OCT-2001 (first entry)  
XX

DE Human polynucleotide SEQ ID NO 1185.

XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
XX peripheral nervous system; neuropathy; central nervous system; CNS;  
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;  
XX leukemia; ss.

OS Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

PD 26-DEC-2000; 2000MO-US34263.

XX 21-JAN-2000; 2000US-0488725.  
XX 25-APR-2000; 2000US-0552317.  
XX 09-JUL-2000; 2000US-0598042.  
XX 19-JUL-2000; 2000US-0620312.  
XX 03-AUG-2000; 2000US-0653450.  
XX 14-SEP-2000; 2000US-0662191.  
XX 19-OCT-2000; 2000US-0693036.  
XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEO INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
XX Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;  
XX Zhao QA, Zhou P, Goodrich R, Drmanac R;  
XX WPI; 2001-442253/47.  
XX P-PDB; AAM39826.

PT Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -

XX Claim 1; SEQ ID NO 1185; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and  
XX the encoded polypeptides (AAM38642-AAM42213) with neurotropic,  
XX immunosuppressant and cytostatic activity. The polynucleotides are useful  
XX in gene therapy. A composition containing a polypeptide or polynucleotide  
XX of the invention may be used to treat diseases of the peripheral nervous  
XX system, such as peripheral nervous injuries, peripheral neuropathy and  
XX localised neuropathies and central nervous system diseases, such as  
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
XX utilisation of the activities such as: Immune system suppression,  
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.

XX Sequence 2003 BP; 311 A; 659 C; 650 G; 383 T; 0 other;

Query Match 36.1%; Score 25.6; DB 22; Length 2003;  
Best Local Similarity 66.1%; Pred. No. 36;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 GCAACCTGTCGACCCATGCGGTCCGACCGACCGACCTGGCGGAGAGACAGC 56  
DB 1953 GCACACTGCCCCCTTCCAGGTGGGTGAAGCCAGCAGCAGGAGGAGGAGATGC 1898

RESULT 43  
ID AAF27736/c  
AAF27736 standard; cDNA; 2004 BP.

AC AAF27736;  
XX

DT 28-MAR-2001 (first entry)  
XX

DE Human transport protein TPPT-36 coding sequence.

XX Human; transport protein; TPPT; transport disorder; metabolic disorder;  
XX neurological disorder; cardiovascular disorder; reproductive disorder;  
XX immune disorder; cancer; ss.

OS Homo sapiens.

XX WO200078953-A2.

XX 28-DEC-2000.

PD 16-JUN-2000; 2000MO-US16668.

XX 17-JUN-1999; 99US-0139923.  
XX 10-AUG-1999; 99US-0148177.  
XX 18-AUG-1999; 99US-0149357.  
XX 28-OCT-1999; 99US-0162287.

XX (INCY-) INCYTE GENOMICS INC.

XX Lal P, Yang J, Yue H, Hillman JL, Tang YT, Bandman O, Burford N;  
XX Baughn MR, Azimzai Y, Lu DAM, Au-Young J, Patterson C;

XX WPI; 2001-041424/05.

XX P-PDB; AAB60116.

PT Isolated polypeptide with a human transport protein sequence is useful  
PT for the diagnosis, prevention and treatment of disorders associated  
PT with the immune, reproductive and cardiovascular systems -

XX Claim 5; Page 161-162; 165pp; English.

XX The present invention provides the protein and coding sequences for 43  
XX novel human transport proteins (designated TPPTs). These can be used in  
XX the diagnosis and treatment of transport, metabolic, neurological,  
XX reproductive, cardiovascular and immune disorders, and cell proliferative  
XX disorders such as cancer.

XX Sequence 2004 BP; 314 A; 659 C; 650 G; 381 T; 0 other;

Query Match 36.1%; Score 25.6; DB 22; Length 2004;  
Best Local Similarity 66.1%; Pred. No. 36;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 GCAACCTGTCGACCCATGCGGTCCGACCGACCGACCTGGCGGAGAGACAGC 56  
DB 1951 GCACACTGCCCCCTTCCAGGTGGGTGAAGCCAGCAGCAGGAGGAGGAGATGC 1896



## RESULT 44

ID AAF32771

AAAF32771 standard; CDNA; 1634 BP.

AC AAF32771;

DT 22-MAR-2001 (first entry)

DE Human secreted protein CDNA #15.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
XX antiviral; anticonvulsant; antibacterial; antifungal; antiparasitic;  
XX cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;  
XX neurological disease; infection; human; secreted protein; ss.

OS Homo sapiens.

PN MO200077197-A1.

PD 21-DEC-2000.

PF 01-JUN-2000; 2000MO-US14934.

PR 11-JUN-1999; 99US-0138599.

PA (HUMA-) HUMAN GENOME SCT INC.

PA (ROSE/) ROSEN C A.

PI Rosen CA, Ruben SM, Komatsoulis GA;

DR MPI: 2001-032312/04.

DR P-PSDB; AAB64563.

PT Isolated nucleic acid molecule encoding a human secreted protein is  
PT used in preventing, treating or ameliorating a medical condition -

PS Claim 1; Page 455; 558pp; English.

XX The invention relates to the isolation of genes AAF32757-F32803 encoding  
XX 47 human secreted proteins AAB64549-B64594. The genes can be used to  
XX generate fusion proteins by linking to the gene for the human  
XX immunoglobulin G Fc portion (SEQID1) for increasing the stability of  
XX the fusion protein as compared to the human protein only. The genes and  
XX proteins are useful for preventing, ameliorating or treating medical  
XX conditions, e.g. by protein or gene therapy. The genes are isolated  
XX from a range of human tissues disclosed in the specification. The  
XX nucleic acids, proteins, antibodies and (ant)agonists are useful in  
XX the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
XX and ovarian cancer, and other cancers of the adrenal gland, bone, bone  
XX marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
XX (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
XX disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
XX colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)  
XX wound healing; (e) neurological diseases e.g. cerebral anoxia and  
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
XX and parasitic infections.

SQ Sequence 1634 BP; 518 A; 329 C; 346 G; 438 T; 3 other;

Query Match

Best Local Similarity 35.8%; Score 25.4; DB 22; Length 1634;

Matches 35; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 20 CGGTCCGACCGCAGCTGGCGGAGACAGCCTGTGCTCCGCG 70

DB 1156 CGCGCAAGACGCTCCAGCCTGGCGAGACAGCAAGACTCCTCCGTC 1206

## RESULT 45

AAA28683

ID AAA28683 standard; DNA; 2853 BP.

AC AAA28683;

DT 29-AUG-2000 (first entry)

DE DNA encoding JEST, a human SWAP70 homologue.

XX JEST; SWAP70; lymphocyte activation protein; T-cell; B-cell; RasGRP;  
XX signaling; transplantation; anti-inflammatory; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 541..2436

FT /tag= a

PN MO200026241-A2.

PD 11-MAY-2000.

PF 28-OCT-1999; 99WO-US25333.

PR 28-OCT-1998; 98US-0106187.

PR 28-OCT-1999; 99US-0106187.

PA (RIGE-) RIGEL PHARM INC.

PI Ferrick DA;

DR MPI: 2000-365573/31.

DR P-PSDB; AAY92816.

PT Novel JEST protein (T-cell SWAP70 homology) used for screening of T-cell  
PT and B-cell activation modulators

PS Disclosure; Fig 1; 58pp; English.

XX JEST (human homologue of SWAP70) and RasGRP (guanyl nucleotide-releasing  
XX protein for the small guanosine triphosphatase Ras) are novel lymphocyte  
XX activation proteins. The JEST protein is involved in the activation of  
XX T-cells and B-cells. RasGRP binds to JEST and SWAP70, and is involved in  
XX B-cell and T-cell activation signaling. Lymphocyte activation proteins  
XX and their modulators are used in transplantation, acute and chronic  
XX inflammatory diseases, and autoimmune treatments. The JEST and RasGRP  
XX polynucleotides are used to express the polypeptides, and as a source of  
XX primers and probes. The polynucleotides may also be used for chromosome  
XX mapping, and for producing transgenic or knockout animals, and for gene  
XX therapy. The methods are used for diagnosing T-cell and B-cell activation  
XX related conditions. The polypeptides are useful for identifying  
XX modulators and for producing antibodies. The antibodies are used for  
XX isolating the protein, in diagnostic assays for a lymphocyte activation  
XX proteins, and in treatment.

SQ Sequence 2853 BP; 656 A; 821 C; 879 G; 497 T; 0 other;

Query Match

Best Local Similarity 35.8%; Score 25.4; DB 21; Length 2853;

Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 10 CCGACCAATGGGTCGAGACCGCAGCTGGCGGAGAGACAGCCTGTGCTCCG 68

DB 493 CGGATCTTAGTGTCAGAGCGCCGCCAGCGGGGCGGCTCAGCCATGGCCTCGC 551

## RESULT 46

ID AAS35884/C

AA35884 standard; DNA; 16018 BP.

AC AAS35884;

DT 17-DEC-2001 (first entry)

XX Human cardiovascular system antigen genomic DNA SEQ ID No 1384.  
DE  
XX  
KW Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;  
KW chicken; sheep; immunosuppressive; ankylosing; vasculitis; dog;  
KW antileukemic; antiproliferative; cytostatic; cardiant; neuroprotective;  
KW cerebroprotective; nocitropic; antibacterial; vitruce; fungicide; cancer;  
KW ophthalmological; vulnery; gene therapy; autoimmune disease; neoplasm;  
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;  
KW cerebrovascular disorder; nervous system disorder; bacterial infection;  
KW fungal infection; viral infection; ocular disorder; endocrine disorder;  
KW gastrointestinal disorder; renal disorder; respiratory disorder;  
KW wound healing; skin aging; organ transplantation; tissue regeneration;  
KW anti-fertility.  
XX  
OS Homo sapiens.  
XX  
PN WO200155321-A2.  
PD  
XX 02-AUG-2001.  
PF  
XX 17-JAN-2001; 2001WO-US01340.  
PR 31-JAN-2000; 2000US-017965.  
PR 04-FEB-2000; 2000US-018028.  
PR 24-FEB-2000; 2000US-018464.  
PR 02-MAR-2000; 2000US-018630.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-020515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226688.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234397.  
PR 25-SEP-2000; 2000US-0234398.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239335.  
PR 13-OCT-2000; 2000US-0239337.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241281.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249300.

PR 01-DEC-2000: 2000US-0250160.  
PR 01-DEC-2000: 2000US-0250391.  
PR 05-DEC-2000: 2000US-0251030.  
PR 05-DEC-2000: 2000US-0251988.  
PR 05-DEC-2000: 2000US-0256719.  
PR 06-DEC-2000: 2000US-0251479.  
PR 08-DEC-2000: 2000US-0251856.  
PR 08-DEC-2000: 2000US-0251868.  
PR 08-DEC-2000: 2000US-0251869.  
PR 08-DEC-2000: 2000US-0251989.  
PR 08-DEC-2000: 2000US-0251990.  
PR 11-DEC-2000: 2000US-0254097.  
PR 05-JAN-2001: 2001US-02539678.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-451930/48.  
DR  
XX  
XX New cardiovascular system related polynucleotides and polypeptides,  
PT useful for diagnosing, treating and/or preventing disorders of the  
PT cardiovascular system -  
XX  
XX  
DS Claim 1; SEQ ID No 1384; 674pp; English.

CC [Sequence35741-AAS356942](#) represent genomic DNA molecules, which encode  
CC the cardiovascularsystem antigen polypeptides of the invention.  
CC Cardiovascular system antigens and their associated polynucleotides are  
CC useful in the diagnosis, treatment and prevention of various types of  
CC disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
CC chickens or sheep. A pathological condition can be determined by  
CC detecting the presence or absence of a mutation in a cardiovascular  
CC system antigen polynucleotide. The treatable disorders include autoimmune  
CC diseases such as rheumatoid arthritis, hyperproliferative disorders such  
CC as neoplasms of the breast or liver, cardiovascular disorders such as  
CC cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,  
CC nervous system disorders such as Alzheimer's disease, infections caused  
CC by bacteria, viruses and fungi, ocular disorders such as corneal  
CC infection, endocrine disorders such as premature labour and infertility,  
CC gastrointestinal disorders such as Crohn's disease, renal disorders such  
CC as glomerulonephritis and respiratory disorders such as asthma and  
CC pleurisy. The polypeptides can also be used to aid wound healing, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, to regenerate tissues and in chemotaxis.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from Wipo  
CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

OY	7	TCTCGGACCCATCGCGTCCGAA	CCGACCCAGCACTCTGGCGGAGAGACAGACCTGTGCGCTC	66
Db	15423	TGCCCCGTGCTTTGGGGGCGAGGAGGCGACGAGGAGGAGCCACAGTCAGTGCCCGG		15364
OY	67	CGACC	71	
Db	15363	GAACC	15359	

RESULT 47	
AA189669	AA189669 standard, cDNA; 402 bp.
XX	
XX	AA189669;
AC	
XX	
DT	06-NOV-2001 (first entry)
DE	
XX	
XX	
Human polynucleotide seq	ID NO 9729

XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;
KW	nervous system disorders; arthritis; inflammation; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200164835-A2.
XX	
PD	07-SEP-2001.
XX	
PF	26-FEB-2001; 2001WO-US04927.
XX	
PR	28-FEB-2000; 2000US-0515126.
PR	18-MAY-2000; 2000US-0577409.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Drmanac RT;
XX	
DR	WPI: 2001-514838/56.
XX	
DR	P-PSDB; AA009738.
XX	
PT	Isolated nucleic acids and polypeptides, useful for preventing
XX	diagnosing and treating e.g. leukaemia, inflammation and immune
XX	disorders -
PS	Claim 1; SEQ ID NO 9729; 1399bp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AA179941-AA193841) and  
CC the encoded proteins (AA000010-AA031910) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines on  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/published\\_pat\\_sequences](http://wipo.int/pub/published_pat_sequences).  
XX  
XX Sequence 402 BP; 90 A; 147 C; 86 G; 79 T; 0 other;

Query Match	34.9%	Score 24.8	DB 22	Length 402
Best Local Similarity	60.3%	Pred. No. 55		
Matches 41: Conservative	0	Mismatches 27	Indels 0	Gaps 0

  

OY	4	ACCTGTCCGACCCATCGCGTCCGAAACCCGACGACCTGTGGCGGAGAGACACCTGTGGC	63
Db	31	ACCTCTGTACCCCTTCTCCCTCCGCGACGCTTACGAGCCACGAGAGCCCTCTGTGTGGC	90
OY	64	CTTCGACC	71
Db	91	CTTCGAGC	98

RESULT	48
AAC77724/c	
ID	AAC77724 standard; cDNA; 2053 BP

DT		08-FEB-2001 (first entry)
XX		
DE		
XX		
KW	Human cancer associated gene sequence SEQ ID NO:118.	
KW		
KW	Human: cancer associated gene; cancer antigen; detection; cancer;	
KW	diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;	
KW	antidiabetic; antistimatic; antirheumatic; antiarthritis; antiviral;	
KW	antiinflammatory; antihypoid; antiallergic; antibacterial; cardiac;	

KW	dermatological; neuroprotective; thrombolytic; coagulant; neurotropic;
KV	vastotropic; antipsoratic; antilanginogenic; gene therapy; inflammation;
KM	immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW	allergic reaction; graft versus host disease; organ rejection;
KV	haemostatic; thrombolytic; cardiovascular disorder; infection;
KM	neurological disease; drug screening; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO20055350-A1.
XX	
PD	21-SEP-2000.
XX	
PF	08-MAR-2000; 2000WO-US05882.
XX	
PR	12-MAR-1999; 99US-0124270.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Rosen CA, Ruben SM;
XX	
DR	WPI: 2000-587533/55.
XX	
DR	P-PSDB; AAB43515.
PT	
PT	Novel isolated nucleic acids comprising sequences encoding peptides
XX	useful for treating or diagnosing e.g. cancer -
PS	Claim 1; Page 703-704; 2352pp; English.

CC AACCT760770 c AAC784448 encode the human cancer associated proteins given  
CC in ABA83398 to ABA84239. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vlnerynary; immunomodulator;  
CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
CC antiinflammatory; antihypoid; antiallergic; antibacterial; antiviral;  
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
CC neutropic; vasotropic; antipsoriatic and antiangiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists form  
CC the present invention may be used to treat immune disorders by activating  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC8457 and ABA84240 represent sequences used in the exemplification of  
CC the present invention.

Query Match	34.9%	Score 24.8	DB 21	Length 2053
Best Local Similarity	60.3%	Pred No. 64		
Matches 41; Conservative	0	Mismatches 27	Indels 0	Gaps 0

4 ACCTTCCGACCCATGGGGTCCGAAACCGACCTGGGCGGGAGAGACAGCTGTGCC 63  
 963 ACCTCTAGCCCCCTCCCTCGGGCAGGCTCAGGCCAGCCAGGAGGCCCTCTGTGGC 904

QY	64	CTCCGACC	71
Db	903	CTCCGACC	896

RESULT 49  
AAZ24407/c  
ID AAZ24407 standard; cDNA; 2190 BP.

AC AAZ24407;

DT 14-FEB-2000 (first entry)

XX	Human bladder tumour cDNA library derived EST 19.
DE	
XX	Expressed sequence tag; human; bladder; tumour; cancer; cytostatic; treatment; gene therapy; EST; ss.
KW	

OS. Homo sapiens.

PN DE19818619-A1

PD 28-OCT-1999.

PF 21-APR-1998; 98DE-1018619.  
XX

PR 21-APR-1998; 98DE-1018619.

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

DR WPI; 1999-612028/53

PT New nucleic acid sequences expressed in bladder tumor tissue, and derived polynucleotides for treatment of bladder tumor and identification

PT of therapeutic agents -  
YY

PS Claim 3; Page 74-75; 132pp; German.  
xy

This invention describes novel polypeptide fragments (I) and the polynucleotides (II) that encode them that are highly expressed in a human bladder tumour and which have cytostatic activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for treatment of bladder cancer, to directly treat this form of cancer (including expression from gene therapy vectors) or are used in a preparation for cancer treatment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AA43360-243309 represent expressed sequence tag (EST) fragments isolated from a human bladder tumour cDNA library which encode the proteins represented in AA166143-166198.

Sequence 2190 BP; 430 A; 623 C; 653 G; 484 T; 0 other;

Query Match	34.9%	Score 24.8	DB 20	Length 2190
Best Local Similarity	60.3%	Pred. No. 65		
Matches 41, Conservative	0	Mismatches 27	Indels 0	Gaps 0

[illegible]

QY	64	CTCCGACC	71
Db	1063	CTCCGAGC	1056

RESULT 50  
AAZ48077/c  
ID AAZ48077 standard; DNA; 4351 BP

AC AAZ48077;

DT 08-MAR-2000 (first entry)

Human insulin like growth factor II exons 7 to 9 nucleotide sequence.

KW Human; IGF-II; insulin-like growth factor II; cell growth modulation;

KW tumour; inhibition; antisense oligonucleotide; phosphorothioate;

KW metastasis; antitumour; antiproliferative; angiogenesis; apoptosis;  
KM tumour cell migration; proliferative disease; atherosclerosis;  
KW psoriasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO955854-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 23-APR-1999; 99WO-CA00323.  
XX  
PR 23-APR-1998; 98US-0082791.  
XX  
PA (GENE-) GENESENSE TECHNOLOGIES INC.  
XX  
PI Wright JA, Young AH, Lee YS;  
XX  
DR WPI; 2000-062027/05.  
XX  
PT Antisense oligonucleotides against mRNA of insulin-like growth factor  
PI II, for treating tumors and other proliferative diseases .  
XX  
PS Disclosure: Fig 11D; 72pp; English.  
XX  
CC AA248041 to AA248070 represent specifically claimed antisense  
CC oligonucleotides (i) complementary to the mRNA of human insulin-like  
CC growth factor II (IGF-II). The present invention also describes a method  
CC for inhibiting growth or metastasis of mammalian tumours by  
CC administering (i). (i) have antitumour and antiproliferative activity,  
CC and inhibits: (i) the autocrine and paracrine functions of IGF-II which  
CC promote tumour-induced angiogenesis and tumour cell migration; and (ii)  
CC autocrine growth of tumour cells, possibly including induction of  
CC apoptosis. (i) may also function as ribozymes. (i) are used for  
CC inhibiting growth and metastasis of mammalian tumours, also: (i) for  
CC treatment of other proliferative diseases, e.g. atherosclerosis and  
CC psoriasis; (ii) when labeled, as probes for detecting IGF-II mRNA; and  
CC (iii) as molecular weight markers. (i) that bind to the 5'-untranslated  
CC region of the foetal transcript (the form present in tumour cells) should  
CC not affect the adult transcript. They are effective against  
CC drug-resistant tumours. The present sequence represents exons 7 to 9 of  
CC the human IGF-II, from the present invention.  
XX  
SQ Sequence 4351 BP: 1073 A; 1431 C; 1053 G; 794 T; 0 other;  
  
Query Match 34.9%; Score 24.8; DB 21; Length 4351;  
Best Local Similarity 60.3%; Pred. No. 69;  
Matches 41; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
  
OY 4 ACCGTTCGACCCATGCGTCCGAACCGACGACTGGCGGAGAGACAGACCTGTGCG 63  
DB 3386 ACCTGTCTAGCCCTTCCTCCGCGCAGCTGAGCCAGGAGCCCTCTCTGTGCG 3327  
OY 64 CTGCGACC 71  
DB 3326 CTGCGACC 3319

Search completed: November 1, 2002, 15:32:02  
Job time : 320 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:18:01 : Search time 45 seconds  
(without alignments)  
387.555 Million cell updates/sec

Title: US-09-626-616-7\_COPY\_354\_424  
Perfect score: 71  
Sequence: 1 GCACCTGTGCGACCATGC.....ACAGCTGTGCGCTCGACC 71

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 328456

Minimum DB seq length: 35

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

Database :

Issued Patents - NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/Backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	71	100.0	1610	US-08-889-108-7	Sequence 7, Appli
2	71	100.0	1610	PCT-US94-10358-7	Sequence 7, Appli
3	69.4	97.7	2160	US-08-188-275A-1	Sequence 1, Appli
4	69.4	97.7	2162	US-09-351-198-1	Sequence 1, Appli
5	69.4	97.7	2162	US-09-113-426-1	Sequence 1, Appli
6	56.6	79.7	1618	US-08-889-108-1	Sequence 1, Appli
7	56.6	79.7	1618	US-08-889-108-1	Sequence 1, Appli
8	56.6	79.7	1618	US-08-889-108-1	Sequence 1, Appli
9	56.6	79.7	1618	US-08-120-601B-1	Sequence 1, Appli
10	56.6	79.7	1618	US-08-120-601B-3	Sequence 1, Appli
11	56.6	79.7	1618	PCT-US94-10358-1	Sequence 3, Appli
12	56.6	79.7	1618	PCT-US94-10358-3	Sequence 3, Appli
13	56.6	79.7	1618	US-08-430-286A-1	Sequence 1, Appli
14	56.6	79.7	1618	US-08-387-707-15	Sequence 13, Appli
15	56.6	79.7	1618	US-09-171-461-1	Sequence 29, Appli
16	56.6	79.7	1618	US-09-171-461-1	Sequence 1, Appli
17	56.6	79.7	1618	US-08-727-688-1	Sequence 1, Appli
18	56.6	79.7	1618	US-08-727-688-1	Sequence 1, Appli
19	56.6	79.7	1618	US-09-020-956-109	Sequence 109, App
20	56.6	79.7	1618	US-09-030-607-109	Sequence 109, App
21	56.6	79.7	1618	US-09-439-313-109	Sequence 109, App
22	56.6	79.7	1618	US-09-129-075-3	Sequence 3, Appli
23	56.6	79.7	1618	US-09-346-237-12	Sequence 12, Appli
24	56.6	79.7	1618	US-08-012-988A-1	Sequence 1, Appli
25	56.6	79.7	1618	US-09-404-650-3	Sequence 1, Appli
26	56.6	79.7	1618	US-09-030-607-195	Sequence 195, App
27	56.6	79.7	1618	US-09-439-313-195	Sequence 195, App

28	23	32.4	1375	2	US-08-468-812-1	Sequence 1, Appli
29	23	32.4	1375	4	US-08-590-563-1	Sequence 1, Appli
30	22.8	32.1	1335	5	PCT-US91-06532-1	Sequence 1, Appli
31	22.8	32.1	50341	1	US-08-247-901C-1	Sequence 1, Appli
32	22.8	32.1	50341	2	US-09-075-904-1	Sequence 1, Appli
33	22.8	32.1	52297	4	US-09-426-436-1	Sequence 1, Appli
34	22.8	32.1	52297	4	US-08-705-557-1	Sequence 1, Appli
35	22.8	32.1	4403765	4	US-09-103-840A-2	Sequence 2, Appli
36	22.8	32.1	4411529	4	US-09-103-840A-1	Sequence 1, Appli
37	22.6	31.8	4732	5	PCT-US93-06251-22	Sequence 22, Appli
38	22.6	31.8	4736	4	US-09-056-105-12	Sequence 12, Appli
39	22.6	31.8	4741	4	US-09-056-105-11	Sequence 11, Appli
40	22.6	31.8	13842	4	US-09-105-537-30	Sequence 30, Appli
41	22.6	31.8	30001	1	US-08-125-468-1	Sequence 1, Appli
42	22.6	31.8	30001	1	US-08-474-933-1	Sequence 1, Appli
43	22.6	31.8	36519	2	US-08-923-137-2	Sequence 2, Appli
44	22.6	31.8	36778	4	US-09-105-537-5	Sequence 5, Appli
45	22.6	31.8	38506	4	US-09-320-878-19	Sequence 19, Appli
46	22.6	31.8	50937	4	US-09-428-517-1	Sequence 1, Appli
47	22.4	31.5	1452	3	US-09-170-331-3	Sequence 3, Appli
48	22.2	31.3	382	2	US-08-967-101-66	Sequence 96, Appli
49	22.2	31.3	382	2	US-08-592-541-96	Sequence 96, Appli
50	22.2	31.3	382	4	US-09-124-658-96	Sequence 96, Appli
51	22.2	31.3	382	4	US-09-127-480-96	Sequence 96, Appli
52	22.2	31.3	382	4	US-08-496-841C-96	Sequence 96, Appli
53	22.2	31.3	3150	4	US-09-522-666-5	Sequence 5, Appli
54	22.2	31.3	5197	2	US-08-131-365B-53	Sequence 53, Appli
55	22.2	31.3	5197	2	US-08-668-123-53	Sequence 53, Appli
56	22.2	31.3	4411529	4	US-09-103-840A-1	Sequence 1, Appli
57	22	31.0	653	4	US-09-439-313-363	Sequence 363, App
58	22	31.0	50937	4	US-09-428-517-1	Sequence 1, Appli
59	21.8	30.7	643	4	US-08-861-774E-53	Sequence 53, Appli
60	21.8	30.7	1024	3	US-08-934-444-3	Sequence 3, Appli
61	21.8	30.7	1024	3	US-09-143-068-3	Sequence 3, Appli
62	21.8	30.7	1024	4	US-09-143-068-3	Sequence 3, Appli
63	21.8	30.7	1024	4	US-09-202-089-3	Sequence 3, Appli
64	21.8	30.7	1211	2	US-08-997-080-40	Sequence 40, Appli
65	21.8	30.7	1211	2	US-08-997-362-40	Sequence 40, Appli
66	21.8	30.7	1211	3	US-08-872-970-40	Sequence 40, Appli
67	21.8	30.7	1211	3	US-09-095-855-40	Sequence 40, Appli
68	21.8	30.7	1211	4	US-08-705-347A-40	Sequence 40, Appli
69	21.8	30.7	1211	4	US-09-324-542-40	Sequence 40, Appli
70	21.8	30.7	3695	4	US-09-211-704A-1	Sequence 1, Appli
71	21.8	30.7	3991	4	US-08-506-296B-3	Sequence 3, Appli
72	21.6	30.4	2742	4	US-09-237-468A-1	Sequence 1, Appli
73	21.6	30.4	3107	2	US-08-813-940-3	Sequence 3, Appli
74	21.6	30.4	3381	4	US-09-009-119-1	Sequence 1, Appli
75	21.6	30.4	3381	4	US-09-371-507-1	Sequence 1, Appli
76	21.6	30.4	3546	1	US-07-951-715A-10	Sequence 10, Appli
77	21.6	30.4	3546	1	US-07-951-715A-12	Sequence 12, Appli
78	21.6	30.4	3546	1	US-07-951-715A-14	Sequence 14, Appli
79	21.6	30.4	3546	2	US-08-455-448A-10	Sequence 10, Appli
80	21.6	30.4	3546	2	US-08-455-448A-12	Sequence 12, Appli
81	21.6	30.4	3546	2	US-08-455-448A-14	Sequence 14, Appli
82	21.6	30.4	3546	3	US-08-455-595A-10	Sequence 10, Appli
83	21.6	30.4	3546	3	US-08-455-595A-12	Sequence 12, Appli
84	21.6	30.4	3546	3	US-08-455-595A-14	Sequence 14, Appli
85	21.6	30.4	3546	3	US-08-455-504B-10	Sequence 10, Appli
86	21.6	30.4	3546	3	US-08-455-504B-12	Sequence 12, Appli
87	21.6	30.4	3546	3	US-08-455-504B-14	Sequence 14, Appli
88	21.6	30.4	3546	3	US-08-455-444-10	Sequence 10, Appli
89	21.6	30.4	3546	3	US-08-455-444-12	Sequence 12, Appli
90	21.6	30.4	3546	3	US-08-455-444-14	Sequence 14, Appli
91	21.6	30.4	3546	4	US-09-547-422-10	Sequence 10, Appli
92	21.6	30.4	3546	4	US-09-547-422-12	Sequence 12, Appli
93	21.6	30.4	3546	4	US-09-547-422-14	Sequence 14, Appli
94	21.6	30.4	4897	6	US-09-547-422-14	Sequence 14, Appli
95	21.6	30.4	35060	6	US-09-814-095-7	Sequence 7, Appli
96	21.6	30.4	4403765	4	US-09-103-840A-2	Sequence 2, Appli
97	21.4	30.1	994	1	US-08-817-997A-1	Sequence 1, Appli
98	21.4	30.1	1107	2	US-08-933-750C-77	Sequence 77, Appli
99	21.4	30.1	1107	3	US-09-234-613-77	Sequence 77, Appli
100	21.4	30.1	2167	2	US-09-067-351-5	Sequence 5, Appli

101	21.4	30.1	2167	4	US-09-360-490-5	Sequence 5, Appl1	c 174	20.6	29.0	6854	4	US-09-194-905-7	Sequence 7, Appl1
c 102	21.4	30.1	2403	2	US-08-700-013B-26	Sequence 26, Appl1	175	20.6	29.0	17612	3	US-08-911-853-29	Sequence 29, Appl1
c 103	21.4	30.1	2817	2	US-08-655-836-4	Sequence 4, Appl1	176	20.6	29.0	17612	4	US-09-479-409-29	Sequence 29, Appl1
c 104	21.4	30.1	2817	2	US-09-020-753-4	Sequence 4, Appl1	177	20.6	29.0	17612	4	US-09-479-453-29	Sequence 29, Appl1
c 105	21.4	30.1	7888	4	US-08-984-709A-49	Sequence 49, Appl1	c 178	20.4	28.7	495	4	US-09-020-956-94	Sequence 94, Appl1
c 106	21.2	29.9	190	4	US-09-437-457-5	Sequence 5, Appl1	c 179	20.4	28.7	495	4	US-09-030-607-94	Sequence 94, Appl1
c 107	21.2	29.9	342	4	US-08-905-223-196	Sequence 196, App	c 180	20.4	28.7	495	4	US-09-439-313-94	Sequence 94, Appl1
c 108	21.2	29.9	702	4	US-08-458-568A-3	Sequence 3, Appl1	c 181	20.4	28.7	503	4	US-08-483-533-7	Sequence 7, Appl1
c 109	21.2	29.9	2639	6	US-07-952-817-8	Sequence 8, Appl1	c 182	20.4	28.7	503	4	US-09-283-471A-7	Sequence 7, Appl1
c 110	21.2	29.9	2639	6	5210025-1	Patent No. 5210025	c 183	20.4	28.7	617	4	US-09-328-111-846	Sequence 846, App
c 111	21.2	29.9	11604	4	US-09-385-028-13	Sequence 13, Appl1	c 184	20.4	28.7	751	1	US-08-474-177-15	Sequence 15, Appl1
c 112	21.2	29.9	12001	4	US-08-458-568A-11	Sequence 11, Appl1	c 185	20.4	28.7	751	1	US-08-487-033-15	Sequence 15, Appl1
c 113	21.2	29.9	15079	4	US-09-385-028-1	Sequence 1, Appl1	c 186	20.4	28.7	751	1	US-08-480-810-15	Sequence 15, Appl1
c 114	21	29.6	351	4	US-09-085-1998-41	Sequence 41, Appl1	c 187	20.4	28.7	751	2	US-08-508-735-15	Sequence 15, Appl1
c 115	21	29.6	641	6	546585-6	Patent No. 546585	c 188	20.4	28.7	751	2	US-08-448-251-15	Sequence 15, Appl1
c 116	21	29.6	777	4	US-08-998-416-212	Sequence 212, App	c 189	20.4	28.7	751	2	US-08-486-047-15	Sequence 15, Appl1
c 117	21	29.6	783	1	US-08-264-861A-11	Sequence 11, Appl1	c 190	20.4	28.7	751	3	US-09-120-130-15	Sequence 15, Appl1
c 118	21	29.6	783	5	PCT-US95-07784-11	Sequence 11, Appl1	c 191	20.4	28.7	751	3	US-09-115-252-15	Sequence 15, Appl1
c 119	21	29.6	1150	1	US-08-264-861A-10	Sequence 10, Appl1	c 192	20.4	28.7	751	3	US-08-986-515-15	Sequence 15, Appl1
c 120	21	29.6	1150	1	PCT-US95-07784-10	Sequence 10, Appl1	c 193	20.4	28.7	751	3	US-09-120-128-15	Sequence 15, Appl1
c 121	21	29.6	1678	6	5223391-1	Patent No. 5223391	c 194	20.4	28.7	751	4	US-09-120-129-15	Sequence 15, Appl1
c 122	21	29.6	2364	2	US-08-981-690-1	Sequence 1, Appl1	c 195	20.4	28.7	751	4	US-09-201-139-15	Sequence 15, Appl1
c 123	21	29.6	2547	3	US-08-508-761B-1	Sequence 1, Appl1	c 196	20.4	28.7	751	4	US-09-120-131-15	Sequence 15, Appl1
c 124	21	29.6	3247	4	US-09-487-368A-3	Sequence 3, Appl1	c 197	20.4	28.7	751	4	US-08-998-416-467	Sequence 467, App
c 125	21	29.6	4622	4	US-08-509-024-6	Sequence 6, Appl1	c 198	20.4	28.7	831	4	US-08-936-075A-65	Sequence 65, Appl1
c 126	21	29.6	4622	4	US-09-333-279-6	Sequence 6, Appl1	c 199	20.4	28.7	986	2	US-08-665-337A-4	Sequence 4, Appl1
c 127	21	29.6	7286	5	PCT-US95-11684-1	Sequence 1, Appl1	c 200	20.4	28.7	1108	5	PCT-US93-03035-1	Sequence 1, Appl1
c 128	20.8	29.3	553	2	US-08-474-020A-14	Sequence 14, Appl1	c 201	20.4	28.7	1165	3	US-09-036-987A-32	Sequence 32, Appl1
c 129	20.8	29.3	573	5	US-08-290-665A-112	Sequence 112, App	c 202	20.4	28.7	1165	4	US-09-370-700-32	Sequence 32, Appl1
c 130	20.8	29.3	573	5	PCT-US95-10398-112	Sequence 112, App	c 203	20.4	28.7	1280	4	US-08-483-533-38	Sequence 38, Appl1
c 131	20.8	29.3	650	1	US-08-229-515A-13	Sequence 13, Appl1	c 204	20.4	28.7	1280	4	US-09-283-471A-38	Sequence 38, Appl1
c 132	20.8	29.3	650	1	US-08-645-865-13	Sequence 13, Appl1	c 205	20.4	28.7	1292	4	US-08-483-533-37	Sequence 37, Appl1
c 133	20.8	29.3	1368	2	US-08-738-172-3	Sequence 3, Appl1	c 206	20.4	28.7	1292	4	US-09-283-471A-37	Sequence 37, Appl1
c 134	20.8	29.3	1521	1	US-08-083-948-14	Sequence 14, Appl1	c 207	20.4	28.7	1300	4	US-08-483-533-39	Sequence 39, Appl1
c 135	20.8	29.3	1521	1	US-08-393-785-14	Sequence 14, Appl1	c 208	20.4	28.7	1300	4	US-09-283-471A-39	Sequence 39, Appl1
c 136	20.8	29.3	1521	1	US-08-475-694-14	Sequence 14, Appl1	c 209	20.4	28.7	1307	4	US-08-483-533-36	Sequence 36, Appl1
c 137	20.8	29.3	1521	1	US-08-712-057-14	Sequence 14, Appl1	c 210	20.4	28.7	1337	4	US-09-283-471A-36	Sequence 36, Appl1
c 138	20.8	29.3	1524	2	US-08-716-942-24	Sequence 24, Appl1	c 211	20.4	28.7	1472	1	US-08-333-565-1	Sequence 1, Appl1
c 139	20.8	29.3	1647	1	US-08-083-948-13	Sequence 13, Appl1	c 212	20.4	28.7	1472	2	US-08-661-479-1	Sequence 1, Appl1
c 140	20.8	29.3	1647	1	US-08-393-785-13	Sequence 13, Appl1	c 213	20.4	28.7	1483	4	US-09-262-749-1	Sequence 1, Appl1
c 141	20.8	29.3	1647	1	US-08-475-694-13	Sequence 13, Appl1	c 214	20.4	28.7	1553	3	US-09-022-669-1	Sequence 1, Appl1
c 142	20.8	29.3	1647	1	US-08-712-057-13	Sequence 13, Appl1	c 215	20.4	28.7	1620	3	US-08-985-950-11	Sequence 11, Appl1
c 143	20.8	29.3	1865	1	US-08-083-948-7	Sequence 7, Appl1	c 216	20.4	28.7	1777	1	US-08-173-508-5	Sequence 5, Appl1
c 144	20.8	29.3	1865	1	US-08-393-785-7	Sequence 7, Appl1	c 217	20.4	28.7	1777	2	US-08-665-310-5	Sequence 5, Appl1
c 145	20.8	29.3	1865	1	US-08-475-694-7	Sequence 7, Appl1	c 218	20.4	28.7	1777	2	US-08-951-712-2	Sequence 2, Appl1
c 146	20.8	29.3	1865	1	US-08-712-057-7	Sequence 7, Appl1	c 219	20.4	28.7	1926	2	US-08-978-182-2	Sequence 2, Appl1
c 147	20.8	29.3	2150	3	US-09-263-023-1	Sequence 1, Appl1	c 220	20.4	28.7	1926	2	US-09-205-681-2	Sequence 2, Appl1
c 148	20.8	29.3	2150	3	US-09-381-849-2	Sequence 1, Appl1	c 221	20.4	28.7	2196	2	US-08-865-337A-2	Sequence 2, Appl1
c 149	20.8	29.3	2774	2	US-08-643-034A-1	Sequence 1, Appl1	c 222	20.4	28.7	5399	1	US-08-368-071-9	Sequence 9, Appl1
c 150	20.8	29.3	2774	3	US-08-648-650A-1	Sequence 1, Appl1	c 223	20.4	28.7	5399	1	US-08-458-181-9	Sequence 9, Appl1
c 151	20.8	29.3	4454	2	US-08-738-172-2	Sequence 2, Appl1	c 224	20.4	28.7	5399	5	PCT-US93-02172-9	Sequence 9, Appl1
c 152	20.8	29.3	4808	2	US-08-231-193A-10	Sequence 10, Appl1	c 225	20.4	28.7	15872	1	US-09-105-537-1	Sequence 1, Appl1
c 153	20.8	29.3	4808	2	US-08-486-273A-10	Sequence 10, Appl1	c 226	20.4	28.7	20235	1	US-07-642-534C-3	Sequence 3, Appl1
c 154	20.8	29.3	4808	3	US-08-940-086A-10	Sequence 10, Appl1	c 227	20.4	28.7	20235	3	US-08-439-009A-3	Sequence 3, Appl1
c 155	20.8	29.3	4808	4	US-08-940-035A-10	Sequence 10, Appl1	c 228	20.4	28.7	335	4	US-09-439-313-391	Sequence 391, App
c 156	20.6	29.0	1289	2	US-08-344-833-1	Sequence 1, Appl1	c 229	20.2	28.5	619	4	US-08-998-416-842	Sequence 842, App
c 157	20.6	29.0	1820	1	US-08-173-508-7	Sequence 7, Appl1	c 230	20.2	28.5	1401	2	US-08-812-412-1	Sequence 1, Appl1
c 158	20.6	29.0	1821	2	US-08-265-310-7	Sequence 7, Appl1	c 231	20.2	28.5	1401	4	US-09-180-271-4	Sequence 4, Appl1
c 159	20.6	29.0	1821	3	US-08-951-742-7	Sequence 7, Appl1	c 232	20.2	28.5	1434	4	US-09-434-288-3	Sequence 3, Appl1
c 160	20.6	29.0	2681	4	US-08-928-213B-7	Sequence 7, Appl1	c 233	20.2	28.5	1596	1	US-08-716-301-11	Sequence 11, Appl1
c 161	20.6	29.0	2742	3	US-08-911-853-16	Sequence 16, Appl1	c 234	20.2	28.5	1596	1	US-09-232-191-36	Sequence 36, Appl1
c 162	20.6	29.0	2742	4	US-09-479-409-16	Sequence 16, Appl1	c 235	20.2	28.5	1794	4	US-09-232-200-90	Sequence 90, Appl1
c 163	20.6	29.0	2742	4	US-09-479-453-16	Sequence 16, Appl1	c 236	20.2	28.5	1794	4	US-09-332-197-90	Sequence 90, Appl1
c 164	20.6	29.0	3000	4	US-09-192-104-1	Sequence 1, Appl1	c 237	20.2	28.5	1794	4	US-09-232-201-90	Sequence 90, Appl1
c 165	20.6	29.0	3000	4	US-09-543-446-1	Sequence 1, Appl1	c 238	20.2	28.5	1882	1	US-08-696-349-1	Sequence 1, Appl1
c 166	20.6	29.0	3003	4	US-08-915-337-1	Sequence 1, Appl1	c 239	20.2	28.5	1882	5	PCT-US96-13156-1	Sequence 1, Appl1
c 167	20.6	29.0	3013	2	US-09-096-982-6	Sequence 6, Appl1	c 240	20.2	28.5	2007	4	US-09-232-191-22	Sequence 22, Appl1
c 168	20.6	29.0	3013	2	US-08-653-650A-6	Sequence 6, Appl1	c 241	20.2	28.5	2007	4	US-09-232-200-22	Sequence 22, Appl1
c 169	20.6	29.0	3572	2	US-08-713-815A-2	Sequence 2, Appl1	c 242	20.2	28.5	2007	4	US-09-232-197-22	Sequence 22, Appl1
c 170	20.6	29.0	3691	4	US-09-211-704A-3	Sequence 3, Appl1	c 243	20.2	28.5	2077	1	US-08-217-327-7	Sequence 7, Appl1
c 171	20.6	29.0	4848	4	US-08-955-957A-1	Sequence 1, Appl1	c 244	20.2	28.5	2077	1	US-08-217-327-7	Sequence 7, Appl1
c 172	20.6	29.0	4848	4	US-08-955-957A-4	Sequence 4, Appl1	c 245	20.2	28.5	3018	3	US-08-942-572-1	Sequence 1, Appl1
c 173	20.6	29.0	4848	4	US-08-955-957A-6	Sequence 6, Appl1	c 246	20.2	28.5	3279	4	US-09-439-313-382	Sequence 382, App



247	20.2	28.5	3411	5	US-08-890-865A-3	Sequence 3, Appli	320	20	28.2	4204	4	US-09-166-448-1	Sequence 1, Appli
248	20.2	28.5	3876	5	PCT-US95-17026-1	Sequence 1, Appli	321	20	28.2	4234	1	US-08-446-038B-1	Sequence 1, Appli
249	20.2	28.5	23673	4	US-09-773-816-1	Sequence 1, Appli	322	20	28.2	4234	1	US-08-446-010B-1	Sequence 1, Appli
C 250	20	28.2	306	4	US-09-199-637A-64	Sequence 64, Appli	323	20	28.2	4234	1	US-08-805-445-1	Sequence 1, Appli
C 251	20	28.2	401	1	US-08-466-033-215	Sequence 215, App	324	20	28.2	4234	2	US-08-064-067D-1	Sequence 1, Appli
C 252	20	28.2	401	1	US-08-444-733-215	Sequence 215, App	325	20	28.2	4234	2	US-09-066-208-1	Sequence 1, Appli
C 253	20	28.2	401	2	US-08-464-134-215	Sequence 215, App	326	20	28.2	4454	2	US-08-738-172-2	Sequence 2, Appli
C 254	20	28.2	401	2	US-08-461-361-215	Sequence 215, App	327	20	28.2	5438	4	US-08-456-200B-5	Sequence 5, Appli
C 255	20	28.2	401	2	US-08-485-910-215	Sequence 215, App	328	20	28.2	8791	5	PCT-US96-01735-5	Sequence 5, Appli
C 256	20	28.2	573	2	US-08-290-665A-110	Sequence 110, App	329	20	28.2	9882	3	US-08-976-255-5	Sequence 5, Appli
C 257	20	28.2	573	5	PCT-US95-10398-110	Sequence 110, App	330	20	28.2	9046	5	US-08-227-536-1	Sequence 1, Appli
258	20	28.2	705	4	US-09-199-637A-60	Sequence 60, Appli	331	20	28.2	9046	5	PCT-US95-04682-1	Sequence 1, Appli
259	20	28.2	721	1	US-08-229-515A-15	Sequence 15, Appli	332	20	28.2	42235	4	US-09-199-637A-1	Sequence 1, Appli
260	20	28.2	721	1	US-08-645-865-15	Sequence 15, Appli	333	20	28.2	49377	4	US-08-764-233A-1	Sequence 1, Appli
261	20	28.2	885	3	US-08-338-368-1	Sequence 1, Appli	C 334	20	28.2	80161	3	US-09-036-987A-1	Sequence 1, Appli
262	20	28.2	1073	3	US-08-356-405-8	Sequence 8, Appli	C 335	20	28.2	80161	4	US-09-370-700-1	Sequence 1, Appli
263	20	28.2	1094	1	US-08-902-294-1	Sequence 1, Appli	19.8	27.9	234	4	US-09-189-060B-46	Sequence 46, Appli	
264	20	28.2	1094	3	US-09-178-637-1	Sequence 1, Appli	19.8	27.9	256	4	US-08-483-533-11	Sequence 11, Appli	
265	20	28.2	1178	2	US-08-107-676-26	Sequence 26, Appli	19.8	27.9	338	3	US-09-283-471A-11	Sequence 11, Appli	
266	20	28.2	1211	2	US-08-107-676-2	Sequence 2, Appli	C 339	19.8	27.9	354	4	US-08-487-761-14	Sequence 14, Appli
C 267	20	28.2	1317	1	US-08-453-472-4	Sequence 4, Appli	340	19.8	27.9	431	4	US-08-483-533-17	Sequence 17, Appli
C 268	20	28.2	1317	1	US-08-038-948-1	Sequence 1, Appli	341	19.8	27.9	431	4	US-09-283-471A-17	Sequence 17, Appli
C 269	20	28.2	1317	1	US-08-453-952-4	Sequence 4, Appli	C 342	19.8	27.9	441	4	US-08-998-416-200	Sequence 200, App
C 270	20	28.2	1317	2	US-08-862-903-4	Sequence 4, Appli	C 343	19.8	27.9	1030	3	US-08-858-003-2	Sequence 2, Appli
C 271	20	28.2	1368	2	US-08-738-172-3	Sequence 3, Appli	C 344	19.8	27.9	1030	3	US-09-078-166-2	Sequence 2, Appli
272	20	28.2	1869	3	US-08-952-967-7	Sequence 7, Appli	C 345	19.8	27.9	1030	3	US-08-997-467-2	Sequence 2, Appli
273	20	28.2	1900	1	US-08-153-848-18	Sequence 18, Appli	346	19.8	27.9	1174	4	US-09-034-985-1	Sequence 1, Appli
274	20	28.2	1900	3	US-09-299-843A-18	Sequence 18, Appli	347	19.8	27.9	1269	5	US-08-265-429A-4	Sequence 4, Appli
275	20	28.2	1900	4	US-09-088-337B-18	Sequence 18, Appli	348	19.8	27.9	1269	5	PCT-US95-09069-4	Sequence 4, Appli
276	20	28.2	1900	5	PCT-US93-11153-18	Sequence 18, Appli	C 349	19.8	27.9	1584	4	US-09-659-166-1	Sequence 1, Appli
277	20	28.2	1947	1	US-07-998-972A-2	Sequence 2, Appli	350	19.8	27.9	1719	4	US-09-042-785A-5	Sequence 5, Appli
278	20	28.2	1947	1	US-08-463-953-2	Sequence 2, Appli	351	19.8	27.9	1724	4	US-09-153-804-8	Sequence 8, Appli
279	20	28.2	1947	1	US-08-462-261-2	Sequence 2, Appli	C 352	19.8	27.9	1946	4	US-09-029-755C-4	Sequence 4, Appli
280	20	28.2	1947	2	US-08-479-733A-24	Sequence 24, Appli	C 353	19.8	27.9	2130	4	US-08-753-247-5	Sequence 5, Appli
281	20	28.2	1947	3	US-08-487-427-24	Sequence 24, Appli	C 354	19.8	27.9	2130	4	US-08-753-247-8	Sequence 8, Appli
282	20	28.2	1947	3	US-08-479-727A-24	Sequence 24, Appli	C 355	19.8	27.9	2151	1	US-08-477-254A-5	Sequence 5, Appli
283	20	28.2	1947	3	US-08-482-369A-24	Sequence 24, Appli	C 356	19.8	27.9	2151	2	US-08-472-576B-5	Sequence 5, Appli
284	20	28.2	1947	5	PCT-US92-11357-2	Sequence 2, Appli	C 357	19.8	27.9	2151	2	US-08-428-734B-5	Sequence 5, Appli
285	20	28.2	1947	5	PCT-US95-07439-24	Sequence 24, Appli	C 358	19.8	27.9	2151	4	US-08-713-556B-5	Sequence 5, Appli
286	20	28.2	1988	1	US-07-750-080A-15	Sequence 15, Appli	C 359	19.8	27.9	2160	4	US-08-753-247-11	Sequence 11, Appli
287	20	28.2	1988	3	US-08-651-472-15	Sequence 15, Appli	C 360	19.8	27.9	2316	2	US-08-714-677-1	Sequence 1, Appli
288	20	28.2	1988	4	US-08-358-928-15	Sequence 15, Appli	C 361	19.8	27.9	2316	2	US-08-393-540-1	Sequence 1, Appli
289	20	28.2	2058	1	US-08-153-848-6	Sequence 6, Appli	C 362	19.8	27.9	2316	2	US-08-714-537-1	Sequence 1, Appli
290	20	28.2	2058	3	US-09-299-843A-6	Sequence 6, Appli	C 363	19.8	27.9	2385	1	US-07-885-972A-1	Sequence 1, Appli
291	20	28.2	2058	4	US-09-088-337B-6	Sequence 6, Appli	C 364	19.8	27.9	2385	2	US-08-745-880-1	Sequence 1, Appli
292	20	28.2	2058	5	PCT-US93-11153-6	Sequence 6, Appli	C 365	19.8	27.9	2385	2	US-08-480-382-1	Sequence 1, Appli
293	20	28.2	2154	1	US-08-383-750-1	Sequence 1, Appli	C 366	19.8	27.9	2475	4	US-09-624-693A-20	Sequence 20, Appli
294	20	28.2	2154	1	US-08-383-751A-1	Sequence 1, Appli	367	19.8	27.9	2745	1	US-08-363-255-1	Sequence 1, Appli
295	20	28.2	2154	3	US-08-352-678-1	Sequence 1, Appli	368	19.8	27.9	2745	1	US-08-363-255-13	Sequence 13, Appli
296	20	28.2	2154	5	PCT-US93-09636-1	Sequence 1, Appli	C 369	19.8	27.9	2877	4	US-09-029-755C-3	Sequence 3, Appli
297	20	28.2	2160	1	US-08-153-848-14	Sequence 14, Appli	C 370	19.8	27.9	2936	2	US-08-714-677-10	Sequence 10, Appli
298	20	28.2	2160	3	US-09-299-843A-14	Sequence 14, Appli	C 371	19.8	27.9	2936	2	US-08-393-540-10	Sequence 10, Appli
299	20	28.2	2160	4	US-09-088-337B-14	Sequence 14, Appli	C 372	19.8	27.9	2936	2	US-08-714-537-10	Sequence 10, Appli
300	20	28.2	2160	5	PCT-US93-11153-14	Sequence 14, Appli	373	19.8	27.9	3061	1	US-09-570-842-1	Sequence 1, Appli
C 301	20	28.2	2310	3	US-09-036-987A-25	Sequence 25, Appli	374	19.8	27.9	3061	1	US-08-700-576-1	Sequence 1, Appli
C 302	20	28.2	2310	4	US-09-370-700-25	Sequence 25, Appli	375	19.8	27.9	3331	4	US-09-042-785A-1	Sequence 1, Appli
C 303	20	28.2	2382	4	US-09-588-256-9	Sequence 9, Appli	376	19.8	27.9	3404	1	US-08-265-429A-1	Sequence 1, Appli
C 304	20	28.2	2600	2	US-08-427-497E-4	Sequence 4, Appli	377	19.8	27.9	3404	5	PCT-US95-09069-1	Sequence 1, Appli
305	20	28.2	2936	2	US-08-738-172-1	Sequence 1, Appli	C 378	19.8	27.9	4200	1	US-07-841-634B-1	Sequence 1, Appli
306	20	28.2	3032	3	US-08-990-140-1	Sequence 1, Appli	C 379	19.8	27.9	4200	1	US-07-946-234A-1	Sequence 1, Appli
307	20	28.2	3032	4	US-09-546-238-1	Sequence 1, Appli	C 380	19.8	27.9	4200	1	US-08-123-161A-1	Sequence 1, Appli
308	20	28.2	3183	3	US-08-427-497E-3	Sequence 3, Appli	C 381	19.8	27.9	4200	5	US-08-483-278-1	Sequence 1, Appli
309	20	28.2	3383	5	PCT-US95-09098-1	Sequence 1, Appli	C 382	19.8	27.9	4200	5	PCT-US93-01560-1	Sequence 1, Appli
310	20	28.2	3429	1	US-08-097-997A-10	Sequence 10, Appli	C 383	19.8	27.9	4405	1	US-07-885-972A-3	Sequence 3, Appli
311	20	28.2	3429	3	US-08-665-574C-10	Sequence 10, Appli	C 384	19.8	27.9	4405	2	US-08-745-880-3	Sequence 3, Appli
312	20	28.2	3429	4	US-08-946-994-10	Sequence 10, Appli	C 385	19.8	27.9	4405	2	US-08-480-382-3	Sequence 3, Appli
C 313	20	28.2	3756	2	US-08-576-626A-1	Sequence 1, Appli	C 386	19.8	27.9	4465	4	US-09-485-636-1	Sequence 1, Appli
314	20	28.2	3774	2	US-08-341-843B-1	Sequence 1, Appli	C 387	19.8	27.9	4465	4	US-09-485-636-1	Sequence 1, Appli
315	20	28.2	3774	2	US-08-427-497E-2	Sequence 2, Appli	388	19.8	27.9	4650	1	US-07-998-003A-102	Sequence 102, App
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317	20	28.2	3888	4	US-08-506-296B-13	Sequence 13, Appli	390	19.8	27.9	4650	1	US-08-268-161A-102	Sequence 102, App
318	20	28.2	4204	2	US-08-928-615-1	Sequence 1, Appli	391	19.8	27.9	4650	1	US-08-268-161A-102	Sequence 102, App
319	20	28.2	4204	4	US-09-056-105-6	Sequence 6, Appli	392	19.8	27.9	4650	2	US-08-453-702A-102	Sequence 102, App

393	19.8	27.9	4650	4	US-09-099-639-102	Sequence 102, App	466	19.6	27.6	3044	3	US-09-139-491-44	Sequence 44, Appl
394	19.8	27.9	4650	5	PCT-US93-12588-102	Sequence 102, App	467	19.6	27.6	3044	2	PCT-US92-03222-44	Sequence 44, Appl
395	19.8	27.9	4650	5	PCT-US95-08071-102	Sequence 102, App	468	19.6	27.6	3382	5	US-08-682-847-1	Sequence 1, Appl
396	19.8	27.9	4655	2	US-08-231-193A-57	Sequence 57, Appl	469	19.6	27.6	3519	1	US-08-035-558-1	Sequence 1, Appl
397	19.8	27.9	4655	2	US-08-486-273A-57	Sequence 57, Appl	470	19.6	27.6	3789	1	US-07-872-644-42	Sequence 42, Appl
398	19.8	27.9	4655	3	US-08-940-086A-57	Sequence 57, Appl	471	19.6	27.6	3789	1	US-08-297-494-42	Sequence 42, Appl
399	19.8	27.9	4655	4	US-08-940-035A-57	Sequence 57, Appl	472	19.6	27.6	3789	1	US-08-297-510-42	Sequence 42, Appl
400	19.8	27.9	4655	3	US-09-181-706-1	Sequence 1, Appl	473	19.6	27.6	3789	1	US-08-479-532-42	Sequence 42, Appl
401	19.8	27.9	4707	4	US-09-459-066-1	Sequence 1, Appl	474	19.6	27.6	3789	1	US-08-455-526-42	Sequence 42, Appl
402	19.8	27.9	4707	4	US-09-459-066-1	Sequence 1, Appl	475	19.6	27.6	3789	1	US-08-455-526-42	Sequence 42, Appl
403	19.8	27.9	5434	2	US-08-841-349-1	Sequence 1, Appl	476	19.6	27.6	3789	5	PCT-US92-03222-42	Sequence 42, Appl
404	19.8	27.9	5538	2	US-08-231-193A-55	Sequence 55, Appl	477	19.6	27.6	3789	5	PCT-US92-03222-42	Sequence 42, Appl
405	19.8	27.9	5538	2	US-08-486-273A-55	Sequence 55, Appl	478	19.6	27.6	4131	1	US-07-872-644-38	Sequence 38, Appl
406	19.8	27.9	5538	3	US-08-940-086A-55	Sequence 55, Appl	479	19.6	27.6	4131	1	US-08-297-494-38	Sequence 38, Appl
407	19.8	27.9	5538	4	US-08-940-035A-55	Sequence 55, Appl	480	19.6	27.6	4131	1	US-08-297-510-38	Sequence 38, Appl
408	19.8	27.9	5605	2	US-09-268-140-6	Sequence 6, Appl	481	19.6	27.6	4131	1	US-08-479-532-38	Sequence 38, Appl
409	19.8	27.9	7785	4	US-08-276-967-1	Sequence 1, Appl	482	19.6	27.6	4131	1	US-08-455-526-38	Sequence 38, Appl
410	19.8	27.9	8252	1	US-08-046-585-15	Sequence 15, Appl	483	19.6	27.6	4131	1	US-08-455-526-38	Sequence 38, Appl
411	19.8	27.9	8252	1	US-08-393-703-15	Sequence 15, Appl	484	19.6	27.6	4131	3	US-09-139-491-38	Sequence 38, Appl
412	19.8	27.9	8252	5	PCT-US93-11721-15	Sequence 15, Appl	485	19.6	27.6	4131	5	PCT-US92-03222-38	Sequence 38, Appl
413	19.8	27.9	9785	4	US-09-479-128-1	Sequence 1, Appl	486	19.6	27.6	4425	1	US-08-222-616-32	Sequence 32, Appl
414	19.8	27.9	30001	1	US-08-125-468-1	Sequence 1, Appl	487	19.6	27.6	4425	5	PCT-US95-04228-32	Sequence 32, Appl
415	19.8	27.9	30001	2	US-08-474-933-1	Sequence 1, Appl	488	19.6	27.6	4451	3	US-08-717-294-42	Sequence 42, Appl
416	19.6	27.6	207	4	US-08-990-823-24	Sequence 24, Appl	489	19.6	27.6	4758	3	US-09-191-647-1	Sequence 1, Appl
417	19.6	27.6	471	2	US-08-883-070-2	Sequence 2, Appl	490	19.6	27.6	4758	4	US-09-540-454-1	Sequence 1, Appl
418	19.6	27.6	484	5	PCT-US95-08295-16	Sequence 16, Appl	491	19.6	27.6	4758	4	US-09-540-454-1	Sequence 1, Appl
419	19.6	27.6	561	5	PCT-US95-06726-35	Sequence 35, Appl	492	19.6	27.6	5996	3	US-09-028-934-33	Sequence 33, Appl
420	19.6	27.6	798	3	US-09-354-129-5	Sequence 5, Appl	493	19.6	27.6	7676	2	US-08-451-778A-7	Sequence 7, Appl
421	19.6	27.6	831	4	US-08-836-075A-65	Sequence 65, Appl	494	19.6	27.6	7676	2	US-08-451-778A-7	Sequence 7, Appl
422	19.6	27.6	969	2	US-08-700-637-1	Sequence 1, Appl	495	19.6	27.6	7676	5	PCT-US95-06743-7	Sequence 7, Appl
423	19.6	27.6	975	4	US-09-365-150-3	Sequence 3, Appl	496	19.6	27.6	7676	5	PCT-US95-06743-7	Sequence 7, Appl
424	19.6	27.6	1073	4	US-09-430-503-25	Sequence 25, Appl	497	19.6	27.6	71989	4	US-09-443-501A-2	Sequence 2, Appl
425	19.6	27.6	1073	4	US-09-430-503-27	Sequence 27, Appl	498	19.4	27.3	210	6	5212296-19	Patent No. 5212296
426	19.6	27.6	1073	4	US-09-430-503-29	Sequence 29, Appl	499	19.4	27.3	217	4	US-09-060-756-558	Sequence 558, App
427	19.6	27.6	1073	4	US-09-430-503-31	Sequence 31, Appl	500	19.4	27.3	337	4	US-09-060-756-244	Sequence 244, App
428	19.6	27.6	1272	3	US-08-946-026-36	Sequence 36, Appl	501	19.4	27.3	369	4	US-09-199-637A-352	Sequence 352, App
429	19.6	27.6	1328	4	US-09-029-333-1	Sequence 1, Appl	502	19.4	27.3	375	4	US-09-199-637A-36	Sequence 36, App
430	19.6	27.6	1330	3	US-08-888-077A-26	Sequence 26, Appl	503	19.4	27.3	491	4	US-09-060-756-107	Sequence 107, App
431	19.6	27.6	1371	3	US-08-462-969A-1	Sequence 1, Appl	504	19.4	27.3	640	2	US-08-403-8520-8	Sequence 8, Appl
432	19.6	27.6	1576	6	5260432-1	Patent No. 5260432	505	19.4	27.3	640	4	US-08-510-646B-8	Sequence 8, Appl
433	19.6	27.6	1679	2	US-09-069-023-35	Sequence 35, Appl	506	19.4	27.3	640	4	US-09-231-818A-8	Sequence 8, Appl
434	19.6	27.6	1753	2	US-08-750-134A-8	Sequence 8, Appl	507	19.4	27.3	659	2	US-08-820-170A-17	Sequence 17, Appl
435	19.6	27.6	1753	2	US-09-363-745-8	Sequence 8, Appl	508	19.4	27.3	659	3	US-09-055-609-17	Sequence 17, Appl
436	19.6	27.6	1844	2	US-08-538-816A-10	Sequence 10, Appl	509	19.4	27.3	659	4	US-09-273-565-17	Sequence 17, Appl
437	19.6	27.6	1844	2	US-09-076-651-10	Sequence 10, Appl	510	19.4	27.3	659	4	US-09-565-538-17	Sequence 17, Appl
438	19.6	27.6	1844	4	US-09-208-394-10	Sequence 10, Appl	511	19.4	27.3	700	4	US-08-991-789A-174	Sequence 174, App
439	19.6	27.6	1894	2	US-08-538-816A-8	Sequence 8, Appl	512	19.4	27.3	700	4	US-09-062-451-174	Sequence 174, App
440	19.6	27.6	1894	4	US-09-076-651-8	Sequence 8, Appl	513	19.4	27.3	830	4	US-08-913-362-1	Sequence 1, Appl
441	19.6	27.6	1894	4	US-09-208-394-8	Sequence 8, Appl	514	19.4	27.3	830	4	US-08-913-362-5	Sequence 5, Appl
442	19.6	27.6	2207	4	US-09-227-357-83	Sequence 83, Appl	515	19.4	27.3	888	4	US-09-199-637A-340	Sequence 340, App
443	19.6	27.6	2207	4	US-08-858-207A-46	Sequence 46, Appl	516	19.4	27.3	1128	2	US-08-820-170A-18	Sequence 18, Appl
444	19.6	27.6	2541	2	US-08-656-393-1	Sequence 1, Appl	517	19.4	27.3	1128	3	US-09-055-609-18	Sequence 18, Appl
445	19.6	27.6	2550	1	US-08-245-295-10	Sequence 10, Appl	518	19.4	27.3	1128	4	US-09-273-565-18	Sequence 18, Appl
446	19.6	27.6	2550	1	US-08-481-130-10	Sequence 10, Appl	519	19.4	27.3	1128	4	US-09-565-538-18	Sequence 18, Appl
447	19.6	27.6	2550	1	US-08-656-984A-10	Sequence 10, Appl	520	19.4	27.3	1128	4	US-09-071-709-7	Sequence 7, Appl
448	19.6	27.6	2550	1	US-08-485-604-10	Sequence 10, Appl	521	19.4	27.3	1271	4	US-09-231-827-1	Sequence 1, Appl
449	19.6	27.6	2550	2	US-08-487-595-10	Sequence 10, Appl	522	19.4	27.3	1342	4	US-09-199-637A-348	Sequence 348, App
450	19.6	27.6	2550	2	US-09-305-640-1	Sequence 1, Appl	523	19.4	27.3	1342	4	US-09-199-637A-350	Sequence 350, App
451	19.6	27.6	2675	2	US-08-883-070-1	Sequence 1, Appl	524	19.4	27.3	1459	2	US-08-824-707-1	Sequence 1, Appl
452	19.6	27.6	2675	2	US-08-883-070-1	Sequence 1, Appl	525	19.4	27.3	1459	2	US-08-824-707-1	Sequence 1, Appl
453	19.6	27.6	2988	1	US-08-481-130-1	Sequence 1, Appl	526	19.4	27.3	1879	6	5212296-5	Patent No. 5212296
454	19.6	27.6	2988	1	US-08-656-984A-1	Sequence 1, Appl	527	19.4	27.3	1947	1	US-09-160-496-4	Sequence 4, Appl
455	19.6	27.6	2988	1	US-08-485-604-1	Sequence 1, Appl	528	19.4	27.3	1947	1	US-07-951-715A-3	Sequence 3, Appl
456	19.6	27.6	2988	2	US-08-487-595-1	Sequence 1, Appl	529	19.4	27.3	1947	2	US-08-459-448A-3	Sequence 3, Appl
457	19.6	27.6	2988	3	US-09-054-368-1	Sequence 1, Appl	530	19.4	27.3	1947	3	US-08-459-448A-3	Sequence 3, Appl
458	19.6	27.6	2988	3	US-09-054-368-1	Sequence 1, Appl	531	19.4	27.3	1947	3	US-08-459-448A-3	Sequence 3, Appl
459	19.6	27.6	2988	4	US-09-056-704-1	Sequence 1, Appl	532	19.4	27.3	1947	3	US-08-459-448A-3	Sequence 3, Appl
460	19.6	27.6	3044	1	US-07-872-644-44	Sequence 44, Appl	533	19.4	27.3	1947	4	US-09-547-422-3	Sequence 3, Appl
461	19.6	27.6	3044	1	US-08-297-494-44	Sequence 44, Appl	534	19.4	27.3	1947	4	US-09-547-422-3	Sequence 3, Appl
462	19.6	27.6	3044	1	US-08-297-510-44	Sequence 44, Appl	535	19.4	27.3	1981	3	US-09-017-706-3	Sequence 3, Appl
463	19.6	27.6	3044	1	US-08-479-532-44	Sequence 44, Appl	536	19.4	27.3	1981	3	US-09-017-706-5	Sequence 5, Appl
464	19.6	27.6	3044	1	US-08-455-526-44	Sequence 44, Appl	537	19.4	27.3	1981	3	US-09-017-706-6	Sequence 6, Appl
465	19.6	27.6	3044	1	US-08-455-525-44	Sequence 44, Appl	538	19.4	27.3	1981	3	US-09-017-706-7	Sequence 7, Appl

C 539	19.4	27.3	1981	3	US-09-017-706-8	Sequence 8, Appli	612	19.2	27.0	323	2	US-08-935-450-9	Sequence 9, Appli
540	19.4	27.3	2007	3	US-08-941-445A-8	Sequence 8, Appli	C 613	19.2	27.0	328	2	US-09-060-756-330	Sequence 330, App
541	19.4	27.3	2085	1	US-08-572-951-2	Sequence 2, Appli	614	19.2	27.0	350	2	US-09-036-089-1	Sequence 1, Appli
C 542	19.4	27.3	2406	1	US-07-689-008-4	Sequence 1, Appli	615	19.2	27.0	350	2	US-09-036-089-2	Sequence 2, Appli
543	19.4	27.3	2520	2	US-08-450-351-1	Sequence 4, Appli	616	19.2	27.0	428	2	US-09-036-089-5	Sequence 5, Appli
544	19.4	27.3	2520	2	US-08-450-351-3	Sequence 3, Appli	617	19.2	27.0	485	2	US-08-403-882D-15	Sequence 15, Appli
545	19.4	27.3	2582	2	US-08-816-105A-2	Sequence 2, Appli	618	19.2	27.0	485	3	US-08-510-646B-15	Sequence 15, Appli
546	19.4	27.3	3014	1	US-08-629-939-1	Sequence 1, Appli	619	19.2	27.0	485	4	US-09-231-818-15	Sequence 15, Appli
547	19.4	27.3	3014	1	US-07-951-873-1	Sequence 1, Appli	620	19.2	27.0	485	4	US-09-085-199B-32	Sequence 32, Appli
548	19.4	27.3	3468	1	US-07-951-715A-2	Sequence 2, Appli	621	19.2	27.0	530	3	US-08-758-662-4	Sequence 4, Appli
549	19.4	27.3	3468	1	US-07-951-715A-4	Sequence 4, Appli	C 622	19.2	27.0	549	3	US-08-441-971-58	Sequence 58, Appli
550	19.4	27.3	3468	1	US-07-951-715A-8	Sequence 8, Appli	C 623	19.2	27.0	549	3	US-08-441-971-59	Sequence 59, Appli
551	19.4	27.3	3468	2	US-08-453-448A-2	Sequence 2, Appli	C 624	19.2	27.0	549	3	US-08-441-971-60	Sequence 60, Appli
552	19.4	27.3	3468	2	US-08-453-448A-8	Sequence 8, Appli	C 625	19.2	27.0	549	4	US-08-221-653-58	Sequence 58, Appli
553	19.4	27.3	3468	2	US-08-453-448A-8	Sequence 8, Appli	C 626	19.2	27.0	549	4	US-08-221-653-59	Sequence 59, Appli
554	19.4	27.3	3468	3	US-08-453-448A-8	Sequence 2, Appli	C 627	19.2	27.0	549	4	US-08-221-653-60	Sequence 60, Appli
555	19.4	27.3	3468	3	US-08-453-448A-2	Sequence 4, Appli	C 628	19.2	27.0	549	4	US-08-442-144A-58	Sequence 58, Appli
556	19.4	27.3	3468	3	US-08-453-448A-8	Sequence 8, Appli	C 629	19.2	27.0	549	4	US-08-442-144A-59	Sequence 59, Appli
557	19.4	27.3	3468	3	US-08-453-504B-2	Sequence 2, Appli	C 630	19.2	27.0	549	4	US-08-441-970-58	Sequence 58, Appli
558	19.4	27.3	3468	3	US-08-453-504B-4	Sequence 4, Appli	C 631	19.2	27.0	549	4	US-08-441-970-59	Sequence 59, Appli
559	19.4	27.3	3468	3	US-08-453-504B-8	Sequence 8, Appli	C 632	19.2	27.0	549	4	US-08-441-970-59	Sequence 60, Appli
560	19.4	27.3	3468	3	US-08-453-444-2	Sequence 2, Appli	C 633	19.2	27.0	549	4	US-08-441-970-60	Sequence 109, App
561	19.4	27.3	3468	3	US-08-453-444-4	Sequence 4, Appli	C 634	19.2	27.0	573	2	US-08-290-665A-109	Sequence 113, App
562	19.4	27.3	3468	3	US-08-453-444-8	Sequence 8, Appli	C 635	19.2	27.0	573	2	US-08-290-665A-113	Sequence 113, App
563	19.4	27.3	3468	3	US-09-033-549-3	Sequence 3, Appli	C 636	19.2	27.0	573	2	US-08-290-665A-115	Sequence 115, App
564	19.4	27.3	3468	3	US-09-033-549-5	Sequence 5, Appli	C 637	19.2	27.0	573	5	PCT-US95-10398-109	Sequence 109, App
565	19.4	27.3	3468	4	US-09-547-442-2	Sequence 2, Appli	C 638	19.2	27.0	573	5	PCT-US95-10398-113	Sequence 115, App
566	19.4	27.3	3468	4	US-09-547-442-2	Sequence 4, Appli	C 639	19.2	27.0	757	5	PCT-US95-10398-115	Sequence 115, App
567	19.4	27.3	3468	4	US-09-547-442-8	Sequence 8, Appli	C 640	19.2	27.0	757	1	US-08-229-515A-10	Sequence 10, Appli
568	19.4	27.3	3546	1	US-07-951-715A-27	Sequence 27, Appli	641	19.2	27.0	757	1	US-08-645-865-10	Sequence 10, Appli
569	19.4	27.3	3546	2	US-08-453-448A-27	Sequence 27, Appli	C 642	19.2	27.0	834	2	US-08-191-160-5	Sequence 5, Appli
570	19.4	27.3	3546	2	US-08-453-595A-27	Sequence 27, Appli	C 643	19.2	27.0	914	2	US-08-935-450-10	Sequence 10, Appli
571	19.4	27.3	3546	3	US-08-453-504B-27	Sequence 27, Appli	C 644	19.2	27.0	1037	1	US-08-462-195-3	Sequence 3, Appli
572	19.4	27.3	3546	3	US-08-453-504B-4	Sequence 4, Appli	C 645	19.2	27.0	1037	2	US-08-636-883-3	Sequence 3, Appli
573	19.4	27.3	3546	4	US-09-547-442-27	Sequence 27, Appli	C 646	19.2	27.0	1037	1	US-09-127-829-3	Sequence 3, Appli
574	19.4	27.3	3547	1	US-07-951-715A-16	Sequence 16, Appli	C 647	19.2	27.0	1167	1	US-08-324-977-9	Sequence 9, Appli
575	19.4	27.3	3547	2	US-08-453-448A-16	Sequence 16, Appli	C 648	19.2	27.0	1167	2	US-08-384-616-9	Sequence 9, Appli
576	19.4	27.3	3547	3	US-08-453-595A-16	Sequence 16, Appli	C 649	19.2	27.0	1167	2	US-08-904-666A-9	Sequence 9, Appli
577	19.4	27.3	3547	3	US-08-453-504B-16	Sequence 16, Appli	C 650	19.2	27.0	1167	2	US-09-315-850-9	Sequence 9, Appli
578	19.4	27.3	3547	3	US-08-453-504B-16	Sequence 16, Appli	C 651	19.2	27.0	1260	4	US-08-949-202-1	Sequence 1, Appli
579	19.4	27.3	3547	4	US-09-547-442-16	Sequence 16, Appli	652	19.2	27.0	1260	4	US-09-418-175-1	Sequence 1, Appli
580	19.4	27.3	3708	2	US-08-680-376-29	Sequence 29, Appli	653	19.2	27.0	1346	3	US-08-949-202-3	Sequence 3, Appli
581	19.4	27.3	4287	1	US-08-244-189-1	Sequence 1, Appli	654	19.2	27.0	1346	4	US-09-418-175-3	Sequence 3, Appli
582	19.4	27.3	4287	1	US-08-306-691B-53	Sequence 53, Appli	C 655	19.2	27.0	1499	2	US-08-324-977-3	Sequence 3, Appli
583	19.4	27.3	4488	4	US-08-406-030A-3	Sequence 3, Appli	C 656	19.2	27.0	1499	2	US-08-384-616-3	Sequence 3, Appli
584	19.4	27.3	4488	6	5183745-1	Patent No. 5183745	C 657	19.2	27.0	1499	2	US-08-904-666A-9	Sequence 3, Appli
C 585	19.4	27.3	5036	4	US-09-177-349-2	Sequence 2, Appli	C 658	19.2	27.0	1499	4	US-09-315-850-3	Sequence 3, Appli
C 586	19.4	27.3	5467	1	US-07-745-206A-12	Sequence 12, Appli	C 659	19.2	27.0	1539	2	US-08-470-426B-17	Sequence 17, Appli
C 587	19.4	27.3	5467	2	US-08-311-363-12	Sequence 12, Appli	660	19.2	27.0	1571	4	US-08-866-435-32	Sequence 32, Appli
C 588	19.4	27.3	6441	4	US-08-669-785-1	Sequence 1, Appli	661	19.2	27.0	1571	4	US-08-744-231-32	Sequence 32, Appli
C 589	19.4	27.3	6441	6	5183745-5	Patent No. 5183745	662	19.2	27.0	1618	2	US-08-533-669A-9	Sequence 9, Appli
C 590	19.4	27.3	7175	1	US-08-455-543A-8	Sequence 8, Appli	663	19.2	27.0	1618	2	US-08-607-509-1	Sequence 1, Appli
C 591	19.4	27.3	7175	2	US-08-193-078B-8	Sequence 8, Appli	664	19.2	27.0	1618	2	US-08-454-036-1	Sequence 1, Appli
C 592	19.4	27.3	7175	2	US-08-223-305C-8	Sequence 8, Appli	665	19.2	27.0	1618	2	US-08-638-642-1	Sequence 1, Appli
C 593	19.4	27.3	7175	2	US-08-149-097D-8	Sequence 8, Appli	666	19.2	27.0	1618	2	US-08-989-370-1	Sequence 1, Appli
C 594	19.4	27.3	7175	3	US-08-949-386-8	Sequence 8, Appli	667	19.2	27.0	1618	5	PCT-US95-05064-1	Sequence 1, Appli
C 595	19.4	27.3	7175	3	US-08-450-562-8	Sequence 8, Appli	668	19.2	27.0	1680	1	US-08-014-723-13	Sequence 13, Appli
C 596	19.4	27.3	7175	4	US-08-984-709A-8	Sequence 8, Appli	C 669	19.2	27.0	1680	1	US-08-014-723-15	Sequence 15, Appli
C 597	19.4	27.3	7362	1	US-08-455-543A-7	Sequence 7, Appli	C 670	19.2	27.0	1680	1	US-08-110-011A-13	Sequence 13, Appli
C 598	19.4	27.3	7362	1	US-08-193-078B-7	Sequence 7, Appli	C 671	19.2	27.0	1680	1	US-08-110-011A-15	Sequence 15, Appli
C 599	19.4	27.3	7362	2	US-08-223-305C-7	Sequence 7, Appli	C 672	19.2	27.0	1734	6	5352575-8	Patent No. 5352575
C 600	19.4	27.3	7362	2	US-08-149-097D-7	Sequence 7, Appli	C 673	19.2	27.0	1758	4	US-09-191-171-6	Sequence 6, Appli
C 601	19.4	27.3	7362	2	US-08-949-386-7	Sequence 7, Appli	C 674	19.2	27.0	1801	5	US-09-385-707-6	Sequence 6, Appli
C 602	19.4	27.3	7362	3	US-08-450-562-7	Sequence 7, Appli	C 675	19.2	27.0	1801	5	PCT-US95-02455-1	Sequence 1, Appli
C 603	19.4	27.3	7362	4	US-08-984-709A-7	Sequence 7, Appli	C 676	19.2	27.0	1863	2	US-08-470-426B-14	Sequence 14, Appli
C 604	19.4	27.3	9540	1	US-07-689-008-1	Sequence 1, Appli	C 677	19.2	27.0	2116	4	US-08-191-160-21	Sequence 21, Appli
C 605	19.4	27.3	13987	2	US-08-804-227C-13	Sequence 13, Appli	C 678	19.2	27.0	2242	4	US-08-464-700-33	Sequence 33, Appli
C 606	19.4	27.3	15297	4	US-09-817-180-3	Sequence 3, Appli	C 679	19.2	27.0	2242	4	US-08-641-627A-37	Sequence 37, Appli
C 607	19.4	27.3	16836	4	US-09-147-236-1	Sequence 1, Appli	C 680	19.2	27.0	2427	2	US-08-678-039A-39	Sequence 39, Appli
C 608	19.4	27.3	16836	4	US-09-147-236-10	Sequence 10, Appli	681	19.2	27.0	2561	4	US-09-146-221-7	Sequence 7, Appli
C 609	19.4	27.3	44377	2	US-08-804-227C-7	Sequence 7, Appli	C 682	19.2	27.0	2952	2	US-08-318-794A-4	Sequence 4, Appli
C 610	19.4	27.3	44377	2	US-08-804-198-1	Sequence 1, Appli	C 683	19.2	27.0	3107	2	US-08-813-940-3	Sequence 3, Appli
C 611	19.2	27.0	298	2	US-09-036-089-4	Sequence 4, Appli	C 684	19.2	27.0	3590	1	US-08-587-889-1	Sequence 1, Appli

C 685	19.2	27.0	3590	5	PCT-US96-09193-1	Sequence 1, Appl1	758	19	26.8	1422	4	US-08-979-608A-13	Sequence 13, Appl1
686	19.2	27.0	4473	2	US-09-048-804-1	Sequence 1, Appl1	C 759	19	26.8	1456	3	US-09-037-135-1	Sequence 1, Appl1
687	19.2	27.0	4473	4	US-09-056-105-26	Sequence 26, Appl1	C 760	19	26.8	1554	3	US-08-045-269C-1	Sequence 1, Appl1
688	19.2	27.0	4524	2	US-08-845-998-7	Sequence 7, Appl1	761	19	26.8	1554	3	US-08-371-680-1	Sequence 1, Appl1
689	19.2	27.0	4524	3	US-09-206-537-7	Sequence 7, Appl1	762	19	26.8	1554	5	PCT-US94-01198-1	Sequence 1, Appl1
690	19.2	27.0	4524	4	US-09-330-854-7	Sequence 7, Appl1	763	19	26.8	1517	4	US-08-979-608A-11	Sequence 11, Appl1
691	19.2	27.0	4530	1	US-08-229-515A-9	Sequence 9, Appl1	764	19	26.8	1828	4	US-09-153-804-3	Sequence 3, Appl1
692	19.2	27.0	4530	1	US-08-645-865-9	Sequence 9, Appl1	765	19	26.8	1839	4	US-09-516-914-6	Sequence 6, Appl1
693	19.2	27.0	4837	1	US-09-629-616-1	Sequence 1, Appl1	766	19	26.8	1862	3	US-08-999-723-1	Sequence 1, Appl1
C 694	19.2	27.0	5455	1	US-08-342-930-1	Sequence 1, Appl1	C 767	19	26.8	1862	4	US-09-434-427-1	Sequence 1, Appl1
C 695	19.2	27.0	6039	1	US-08-324-977-11	Sequence 11, Appl1	C 768	19	26.8	1933	3	US-08-974-380-1	Sequence 1, Appl1
C 696	19.2	27.0	6039	2	US-08-384-616-11	Sequence 11, Appl1	769	19	26.8	2037	2	US-08-535-276-1	Sequence 1, Appl1
C 697	19.2	27.0	6039	2	US-08-904-686A-11	Sequence 11, Appl1	770	19	26.8	2138	3	US-08-776-271-1	Sequence 1, Appl1
C 698	19.2	27.0	6039	4	US-09-315-850-11	Sequence 11, Appl1	771	19	26.8	2138	3	US-09-215-035-1	Sequence 1, Appl1
699	19.2	27.0	6503	4	US-09-404-650-12	Sequence 12, Appl1	772	19	26.8	2267	4	US-08-679-645-25	Sequence 25, Appl1
C 700	19.2	27.0	6709	4	US-09-285-601-3	Sequence 3, Appl1	C 773	19	26.8	2278	1	US-08-258-188-1	Sequence 1, Appl1
C 701	19.2	27.0	9030	1	US-08-324-977-13	Sequence 13, Appl1	C 774	19	26.8	2278	1	US-08-526-813-1	Sequence 1, Appl1
C 702	19.2	27.0	9030	2	US-08-384-616-13	Sequence 13, Appl1	C 775	19	26.8	2278	5	PCT-US95-08554-1	Sequence 1, Appl1
C 703	19.2	27.0	9030	2	US-08-904-686A-13	Sequence 13, Appl1	C 776	19	26.8	2388	2	US-08-796-414B-6	Sequence 6, Appl1
C 704	19.2	27.0	9030	4	US-09-315-850-13	Sequence 13, Appl1	C 777	19	26.8	2936	2	US-08-738-172-1	Sequence 1, Appl1
C 705	19.2	27.0	9058	4	US-08-913-014A-9	Sequence 9, Appl1	778	19	26.8	3810	2	US-08-475-844-8	Sequence 8, Appl1
C 706	19.2	27.0	9416	1	US-08-324-977-1	Sequence 1, Appl1	779	19	26.8	3810	5	PCT-US95-08429-8	Sequence 8, Appl1
C 707	19.2	27.0	9416	2	US-08-384-616-1	Sequence 1, Appl1	780	19	26.8	4425	1	US-08-222-616-32	Sequence 32, Appl1
C 708	19.2	27.0	9416	2	US-08-904-686A-1	Sequence 1, Appl1	781	19	26.8	4425	5	PCT-US95-04228-32	Sequence 32, Appl1
C 709	19.2	27.0	9416	4	US-09-315-850-1	Sequence 1, Appl1	782	19	26.8	4496	4	US-08-765-907A-6	Sequence 6, Appl1
C 710	19.2	27.0	9595	3	US-09-014-416-4	Sequence 4, Appl1	C 783	19	26.8	5437	1	US-07-661-610C-1	Sequence 1, Appl1
C 711	19.2	27.0	9599	3	US-09-014-416-6	Sequence 6, Appl1	C 784	19	26.8	5515	4	US-09-398-193-98	Sequence 98, Appl1
C 712	19.2	27.0	13987	2	US-08-804-227C-13	Sequence 13, Appl1	C 785	19	26.8	5515	1	US-08-920-812-23	Sequence 23, Appl1
713	19.2	27.0	14272	4	US-09-516-914-23	Sequence 23, Appl1	786	19	26.8	5975	1	US-08-820-827-23	Sequence 23, Appl1
714	19.2	27.0	36741	4	US-09-301-665-3	Sequence 3, Appl1	787	19	26.8	5975	1	US-08-921-177-23	Sequence 23, Appl1
C 715	19.2	27.0	44377	2	US-08-804-227C-7	Sequence 7, Appl1	788	19	26.8	5975	1	US-08-920-828-23	Sequence 23, Appl1
C 716	19.2	27.0	44377	2	US-08-804-198-1	Sequence 1, Appl1	789	19	26.8	5975	2	US-08-920-828-23	Sequence 23, Appl1
717	19.2	27.0	49377	1	US-08-764-233A-1	Sequence 1, Appl1	790	19	26.8	6235	4	US-09-305-384-5	Sequence 5, Appl1
C 718	19.2	27.0	68750	3	US-09-335-409-1	Sequence 1, Appl1	791	19	26.8	6529	4	US-08-789-329C-1	Sequence 1, Appl1
C 719	19.2	27.0	68750	4	US-09-568-102-1	Sequence 1, Appl1	792	19	26.8	6679	4	US-09-305-384-1	Sequence 1, Appl1
C 720	19.2	27.0	68750	4	US-09-567-969-1	Sequence 1, Appl1	793	19	26.8	6911	1	US-08-311-174-4	Sequence 4, Appl1
C 721	19.2	27.0	68750	4	US-09-568-480-1	Sequence 1, Appl1	794	19	26.8	7824	4	US-08-718-388-6	Sequence 6, Appl1
C 722	19.2	27.0	68750	4	US-09-568-486-1	Sequence 1, Appl1	795	19	26.8	8201	1	US-08-253-155A-9	Sequence 9, Appl1
C 723	19.2	27.0	68750	4	US-09-568-472-1	Sequence 1, Appl1	C 796	19	26.8	961	4	US-08-934-386-7	Sequence 7, Appl1
724	19.2	26.8	231	4	US-09-439-313-459	Sequence 459, App	C 797	19	26.8	10095	3	US-08-822-586-45	Sequence 45, Appl1
725	19.2	26.8	248	4	US-09-007-005-32	Sequence 32, Appl1	C 798	19	26.8	10763	2	US-08-761-258-1	Sequence 1, Appl1
726	19.2	26.8	248	4	US-09-244-796-32	Sequence 32, Appl1	C 799	19	26.8	10763	2	US-08-977-306-1	Sequence 1, Appl1
727	19.2	26.8	277	4	US-09-007-005-3	Sequence 3, Appl1	C 800	19	26.8	11558	4	US-09-134-246-8	Sequence 8, Appl1
728	19.2	26.8	277	4	US-09-244-796-3	Sequence 3, Appl1	C 801	19	26.8	13842	4	US-09-105-537-30	Sequence 30, Appl1
C 729	19.2	26.8	705	4	US-08-998-416-1059	Sequence 1059, Ap	C 802	19	26.8	16382	4	US-08-718-388-8	Sequence 8, Appl1
730	19.2	26.8	806	3	US-09-154-083-7	Sequence 7, Appl1	803	19	26.8	35060	3	US-08-814-095-7	Sequence 7, Appl1
731	19.2	26.8	1010	4	US-08-991-789A-5	Sequence 5, Appl1	C 804	19	26.8	38506	3	US-09-105-537-5	Sequence 5, Appl1
732	19.2	26.8	1010	4	US-09-062-451-5	Sequence 5, Appl1	C 805	19	26.8	50341	1	US-08-320-878-19	Sequence 19, Appl1
733	19.2	26.8	1074	1	US-08-045-269C-3	Sequence 3, Appl1	806	19	26.8	50341	1	US-08-247-901C-1	Sequence 1, Appl1
734	19.2	26.8	1074	3	PCT-US94-01198-3	Sequence 3, Appl1	807	19	26.8	50341	2	US-09-426-436-1	Sequence 1, Appl1
735	19.2	26.8	1080	3	US-09-043-627-1	Sequence 1, Appl1	808	19	26.8	52297	4	US-08-705-557-1	Sequence 1, Appl1
736	19.2	26.8	1194	4	US-08-765-907A-9	Sequence 9, Appl1	809	19	26.8	52297	4	US-08-210-222-11	Sequence 11, Appl1
737	19.2	26.8	1248	4	US-09-232-200-54	Sequence 54, Appl1	810	18.8	26.5	97	1	US-09-060-756-209	Sequence 209, App
738	19.2	26.8	1248	4	US-09-232-197-54	Sequence 54, Appl1	811	18.8	26.5	236	4	US-08-981-189B-16	Sequence 16, Appl1
739	19.2	26.8	1248	4	US-09-332-197-54	Sequence 54, Appl1	812	18.8	26.5	375	4	US-09-086-483A-15	Sequence 15, Appl1
740	19.2	26.8	1252	4	US-09-305-384-7	Sequence 7, Appl1	813	18.8	26.5	398	4	US-08-821-009-2	Sequence 2, Appl1
741	19.2	26.8	1278	4	US-09-232-191-18	Sequence 18, Appl1	814	18.8	26.5	461	2	US-09-099-572-2	Sequence 2, Appl1
742	19.2	26.8	1278	4	US-09-232-191-18	Sequence 18, Appl1	815	18.8	26.5	541	4	US-09-134-246-7	Sequence 4, Appl1
743	19.2	26.8	1278	4	US-09-232-197-18	Sequence 18, Appl1	C 816	18.8	26.5	603	4	US-08-461-052-5	Sequence 5, Appl1
744	19.2	26.8	1278	4	US-09-232-201-18	Sequence 18, Appl1	817	18.8	26.5	603	4	US-08-461-052-5	Sequence 5, Appl1
745	19.2	26.8	1278	4	US-09-232-201-18	Sequence 18, Appl1	818	18.8	26.5	630	3	US-08-689-411-5	Sequence 5, Appl1
C 746	19.2	26.8	1299	1	US-07-661-610C-11	Sequence 11, Appl1	819	18.8	26.5	650	4	US-08-689-411-5	Sequence 5, Appl1
747	19.2	26.8	1336	4	US-08-718-388-2	Sequence 2, Appl1	820	18.8	26.5	650	4	US-08-818-112-141	Sequence 141, App
748	19.2	26.8	1352	1	US-08-233-609-2	Sequence 2, Appl1	821	18.8	26.5	655	4	US-08-818-112-141	Sequence 141, App
749	19.2	26.8	1352	1	US-08-444-083-2	Sequence 2, Appl1	822	18.8	26.5	655	4	US-09-056-556-141	Sequence 141, App
750	19.2	26.8	1352	1	US-08-286-304-2	Sequence 2, Appl1	823	18.8	26.5	655	4	US-09-129-030-41	Sequence 41, Appl1
751	19.2	26.8	1352	1	US-08-442-745-2	Sequence 2, Appl1	C 824	18.8	26.5	664	4	US-09-328-111-279	Sequence 279, App
752	19.2	26.8	1352	1	US-08-443-129-2	Sequence 2, Appl1	825	18.8	26.5	712	2	US-08-747-536-3	Sequence 3, Appl1
753	19.2	26.8	1352	1	US-08-443-952-2	Sequence 2, Appl1	826	18.8	26.5	712	2	US-08-747-536-3	Sequence 3, Appl1
754	19.2	26.8	1352	1	US-08-443-130-2	Sequence 2, Appl1	827	18.8	26.5	722	2	US-08-747-536-7	Sequence 7, Appl1
755	19.2	26.8	1352	5	US-08-898-911-2	Sequence 2, Appl1	828	18.8	26.5	722	2	US-08-702-809A-1	Sequence 1, Appl1
756	19.2	26.8	1352	5	PCT-US95-04467-2	Sequence 12, Appl1	829	18.8	26.5	787	3	US-08-545-809A-14	Sequence 14, Appl1
757	19.2	26.8	1362	4	US-08-979-608A-12	Sequence 12, Appl1	830	18.8	26.5	816	3		

831	18.8	26.5	1024	6	5169835-16	Patent No. 5169835	904	18.8	26.5	6256	2	US-08-587-680A-1	Sequence 1, Appl1
832	18.8	26.5	1071	2	US-08-997-080-180	Sequence 180, App	C 905	18.8	26.5	6756	1	US-08-151-574-31	Sequence 31, Appl1
833	18.8	26.5	1071	2	US-08-997-362-180	Sequence 180, App	C 905	18.8	26.5	6756	2	US-08-419-48-18	Sequence 31, Appl1
834	18.8	26.5	1071	4	US-09-095-855-180	Sequence 180, App	C 907	18.8	26.5	6756	4	US-09-233-510-31	Sequence 31, Appl1
835	18.8	26.5	1071	4	US-09-324-542-180	Sequence 180, App	C 908	18.8	26.5	8460	1	US-08-469-005A-9	Sequence 9, Appl1
836	18.8	26.5	1080	2	US-09-205-922-1	Sequence 1, Appl1	C 909	18.8	26.5	8519	4	US-09-261-907-1	Sequence 1, Appl1
837	18.8	26.5	1212	6	5212296-17	Patent No. 5212296	C 910	18.8	26.5	9540	1	US-07-689-008-1	Sequence 9, Appl1
838	18.8	26.5	1217	2	US-08-846-762-100	Sequence 100, App	C 911	18.8	26.5	11495	4	US-09-056-105-9	Sequence 1, Appl1
839	18.8	26.5	1339	3	US-08-468-856B-3	Sequence 3, Appl1	C 912	18.8	26.5	11958	4	US-09-134-246-8	Sequence 8, Appl1
840	18.8	26.5	1339	3	US-08-468-859A-3	Sequence 3, Appl1	C 913	18.8	26.5	12412	1	US-08-390-878-18	Sequence 18, Appl1
841	18.8	26.5	1345	1	US-08-362-670B-33	Sequence 33, Appl1	C 914	18.8	26.5	16885	1	US-08-390-878-16	Sequence 16, Appl1
842	18.8	26.5	1345	4	US-08-333-576C-33	Sequence 33, Appl1	C 915	18.8	26.5	35100	2	US-08-770-379-19	Sequence 19, Appl1
843	18.8	26.5	1345	4	US-08-808-324-33	Sequence 33, Appl1	C 916	18.8	26.5	35100	4	US-08-757-662A-19	Sequence 19, Appl1
844	18.8	26.5	1345	5	PCT-US94-14030A-33	Sequence 33, Appl1	C 917	18.8	26.5	35100	4	US-09-230-372A-19	Sequence 19, Appl1
C 845	18.8	26.5	1443	3	US-08-959-381A-3	Sequence 3, Appl1	C 918	18.8	26.5	35109	3	US-08-923-137-2	Sequence 2, Appl1
846	18.8	26.5	1473	2	US-08-602-725-31	Sequence 31, Appl1	C 919	18.8	26.5	49272	1	US-08-614-770A-1	Sequence 1, Appl1
847	18.8	26.5	1487	3	US-08-702-609A-3	Sequence 3, Appl1	C 920	18.6	26.2	69	5	PCT-US94-06079-36	Sequence 36, Appl1
848	18.8	26.5	1503	4	US-09-463-702A-33	Sequence 33, Appl1	C 921	18.6	26.2	81	1	US-08-009-265-9	Sequence 9, Appl1
849	18.8	26.5	1535	3	US-08-464-052-1	Sequence 1, Appl1	C 922	18.6	26.2	96	1	US-08-009-265-40	Sequence 40, Appl1
850	18.8	26.5	1535	4	US-08-461-002-1	Sequence 1, Appl1	C 923	18.6	26.2	405	4	US-09-060-756-675	Sequence 675, App
851	18.8	26.5	1535	4	US-08-689-411-1	Sequence 1, Appl1	C 924	18.6	26.2	414	3	US-08-804-180C-1	Sequence 1, Appl1
C 852	18.8	26.5	1535	5	PCT-US94-09863-1	Sequence 1, Appl1	C 925	18.6	26.2	423	4	US-09-144-085-5	Sequence 5, Appl1
C 853	18.8	26.5	1626	3	US-08-959-381A-4	Sequence 4, Appl1	C 926	18.6	26.2	474	2	US-08-653-402B-5	Sequence 5, Appl1
C 854	18.8	26.5	1630	3	US-08-468-856B-2	Sequence 2, Appl1	C 927	18.6	26.2	474	2	US-08-653-402B-9	Sequence 9, Appl1
C 855	18.8	26.5	1630	3	US-08-468-859A-2	Sequence 2, Appl1	C 928	18.6	26.2	561	1	US-08-067-684-13	Sequence 13, Appl1
C 856	18.8	26.5	1813	2	US-08-007-107-1	Sequence 1, Appl1	C 929	18.6	26.2	561	1	US-08-008-898-13	Sequence 13, Appl1
C 857	18.8	26.5	1863	3	US-09-199-229-1	Sequence 1, Appl1	C 930	18.6	26.2	561	2	US-08-459-818-13	Sequence 13, Appl1
C 858	18.8	26.5	1863	3	US-09-443-087-1	Sequence 1, Appl1	C 931	18.6	26.2	561	2	US-08-889-666-13	Sequence 13, Appl1
C 859	18.8	26.5	1863	4	US-09-687-298-1	Sequence 1, Appl1	C 932	18.6	26.2	561	2	US-08-465-078-13	Sequence 13, Appl1
C 860	18.8	26.5	1870	4	US-09-071-709-6	Sequence 6, Appl1	C 933	18.6	26.2	561	2	US-08-725-776-13	Sequence 13, Appl1
C 861	18.8	26.5	1896	4	US-09-345-468-24	Sequence 24, Appl1	C 934	18.6	26.2	561	2	US-08-488-062-13	Sequence 13, Appl1
C 862	18.8	26.5	1998	6	5212296-8	Patent No. 5212296	C 935	18.6	26.2	724	4	US-08-228-208A-13	Sequence 13, Appl1
C 863	18.8	26.5	2170	4	US-09-345-468-11	Sequence 11, Appl1	C 936	18.6	26.2	781	2	US-08-998-416-694	Sequence 694, App
C 864	18.8	26.5	2185	1	US-08-173-508-3	Sequence 3, Appl1	C 937	18.6	26.2	781	2	US-08-459-818-18	Sequence 18, Appl1
C 865	18.8	26.5	2185	2	US-08-265-310-3	Sequence 3, Appl1	C 938	18.6	26.2	781	2	US-08-889-666-18	Sequence 18, Appl1
C 866	18.8	26.5	2185	3	US-08-951-742-3	Sequence 3, Appl1	C 939	18.6	26.2	781	2	US-08-465-078-18	Sequence 18, Appl1
C 867	18.8	26.5	2190	3	US-08-508-761B-5	Sequence 5, Appl1	C 940	18.6	26.2	781	2	US-08-725-776-18	Sequence 18, Appl1
C 868	18.8	26.5	2197	3	US-08-985-950-13	Sequence 13, Appl1	C 941	18.6	26.2	781	2	US-08-488-062-18	Sequence 18, Appl1
C 869	18.8	26.5	2200	3	US-08-985-950-19	Sequence 19, Appl1	C 942	18.6	26.2	837	2	US-08-306-511A-3	Sequence 3, Appl1
C 870	18.8	26.5	2238	1	US-07-841-651-1	Sequence 1, Appl1	C 943	18.6	26.2	837	2	US-08-893-274-3	Sequence 3, Appl1
C 871	18.8	26.5	2251	4	US-08-871-572B-3	Sequence 3, Appl1	C 944	18.6	26.2	850	2	US-08-627-610-3	Sequence 3, Appl1
C 872	18.8	26.5	2271	3	US-08-985-950-15	Sequence 15, Appl1	C 945	18.6	26.2	850	4	US-08-581-918A-3	Sequence 3, Appl1
C 873	18.8	26.5	2375	2	US-08-903-800A-5	Sequence 5, Appl1	C 946	18.6	26.2	850	4	US-08-346-147B-3	Sequence 3, Appl1
C 874	18.8	26.5	2388	3	US-08-985-950-17	Sequence 17, Appl1	C 947	18.6	26.2	850	4	US-08-822-936-3	Sequence 3, Appl1
C 875	18.8	26.5	2401	3	US-09-320-878-20	Sequence 20, Appl1	C 948	18.6	26.2	850	5	PCT-US95-04656-3	Sequence 3, Appl1
C 876	18.8	26.5	2406	1	US-07-689-008-4	Sequence 4, Appl1	C 949	18.6	26.2	861	4	US-08-998-416-299	Sequence 299, App
C 877	18.8	26.5	2461	1	US-08-282-141-1	Sequence 1, Appl1	C 950	18.6	26.2	1021	2	US-08-459-818-17	Sequence 17, Appl1
C 878	18.8	26.5	2874	3	US-08-702-609A-5	Sequence 5, Appl1	C 951	18.6	26.2	1021	2	US-08-889-666-17	Sequence 17, Appl1
C 879	18.8	26.5	2899	4	US-08-981-392-24	Sequence 24, Appl1	C 952	18.6	26.2	1021	2	US-08-465-078-17	Sequence 17, Appl1
C 880	18.8	26.5	3173	3	US-08-468-856B-1	Sequence 1, Appl1	C 953	18.6	26.2	1021	2	US-08-725-776-17	Sequence 17, Appl1
C 881	18.8	26.5	3173	3	US-08-468-859A-1	Sequence 1, Appl1	C 954	18.6	26.2	1021	2	US-08-488-062-17	Sequence 17, Appl1
C 882	18.8	26.5	3231	5	US-08-074-121-4	Sequence 4, Appl1	C 955	18.6	26.2	1035	1	US-08-891-254-8	Sequence 8, Appl1
C 883	18.8	26.5	3231	5	PCT-US94-06447-4	Sequence 4, Appl1	C 956	18.6	26.2	1035	2	US-08-819-539-8	Sequence 8, Appl1
C 884	18.8	26.5	3241	4	US-09-434-288-11	Sequence 11, Appl1	C 957	18.6	26.2	1035	4	US-09-030-270A-8	Sequence 8, Appl1
C 885	18.8	26.5	3461	3	US-08-468-856B-6	Sequence 6, Appl1	C 958	18.6	26.2	1035	4	US-08-984-207-8	Sequence 8, Appl1
C 886	18.8	26.5	3461	3	US-08-468-859A-6	Sequence 6, Appl1	C 959	18.6	26.2	1035	4	US-09-013-587-8	Sequence 8, Appl1
C 887	18.8	26.5	3850	4	US-09-463-702A-1	Sequence 1, Appl1	C 960	18.6	26.2	1035	5	PCT-US96-08819-8	Sequence 8, Appl1
C 888	18.8	26.5	3924	2	US-08-996-644-3	Sequence 3, Appl1	C 961	18.6	26.2	1058	1	US-08-608-241-3	Sequence 3, Appl1
C 889	18.8	26.5	3924	3	US-09-352-552-3	Sequence 3, Appl1	C 962	18.6	26.2	1058	1	US-08-922-182-3	Sequence 3, Appl1
C 890	18.8	26.5	3927	2	US-08-996-644-1	Sequence 1, Appl1	C 963	18.6	26.2	1058	2	US-08-919-953-3	Sequence 3, Appl1
C 891	18.8	26.5	3927	2	US-09-352-552-1	Sequence 1, Appl1	C 964	18.6	26.2	1125	2	US-08-997-080-13	Sequence 13, App
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C 893	18.8	26.5	4884	1	US-07-665-792E-10	Sequence 10, Appl1	C 966	18.6	26.2	1125	4	US-09-095-885-153	Sequence 153, App
C 894	18.8	26.5	5228	4	US-09-428-711A-15	Sequence 15, Appl1	C 967	18.6	26.2	1125	4	US-09-324-542-133	Sequence 153, App
C 895	18.8	26.5	5484	4	US-09-632-580A-3	Sequence 3, Appl1	C 968	18.6	26.2	1135	2	US-08-387-942C-7	Sequence 7, Appl1
C 896	18.8	26.5	5494	4	US-08-910-864-10	Sequence 10, Appl1	C 969	18.6	26.2	1245	1	US-09-337-913-2	Sequence 2, Appl1
C 897	18.8	26.5	5501	1	US-08-484-438-1	Sequence 1, Appl1	C 970	18.6	26.2	1245	4	US-08-750-524-2	Sequence 2, Appl1
C 898	18.8	26.5	5510	1	US-08-123-161A-7	Sequence 7, Appl1	C 971	18.6	26.2	1336	2	US-08-718-388-2	Sequence 2, Appl1
C 899	18.8	26.5	5510	1	US-08-483-278-7	Sequence 7, Appl1	C 972	18.6	26.2	1362	2	US-08-318-837-8	Sequence 8, Appl1
C 900	18.8	26.5	5532	2	US-08-475-035-3	Sequence 3, Appl1	C 973	18.6	26.2	1430	6	5514590-1	Patent No. 5514590
C 901	18.8	26.5	5553	1	US-08-484-438-3	Sequence 3, Appl1	C 974	18.6	26.2	1521	4	US-09-004-502-2	Sequence 2, Appl1
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C 903	18.8	26.5	6256	2	US-08-567-375-1	Sequence 1, Appl1	C 976	18.6	26.2	1560	2	US-08-752-891-1	Sequence 1, Appl1



```

; APPLICANT: Uhl, George R.
; APPLICANT: Wang, Jia-Bei
; APPLICANT: Johnson, Peter S.
; APPLICANT: Persico, Antonio
; TITLE OF INVENTION: cDNA and Genomic Clones Encoding Human
; TITLE OF INVENTION: Mu Opiate Receptor and the Purified Gene Product
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-3487
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,275A
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1173-449P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2160 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2160
; OTHER INFORMATION:
; OTHER INFORMATION: /note="cDNA encoding human mu opiate receptor"
US-08-188-275A-1

Query Match          97.7%; Score 69.4; DB 4; Length 2160;
Best Local Similarity 98.6%; Pred. No. 1.7e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCACCTGTGCCAGCCATGCGTCCGAACCGCAGCAGCCTGCGGCGGAGAGACAGCCTGT 60
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DB 328 GCACCTGTGCCAGCCATGCGTCCGAACCGCAGCAGCAGCCTGCT 387

QY 61 GCCCTCCGACC 71
    |||||||
DB 388 GCCCTCCGACC 398

RESULT 4
US-09-351-198-1
; Sequence 1, Application US/09351198
; Patent No. 6335168
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary J
; APPLICANT: Laforge, Karl S
; APPLICANT: Yu, Lei
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: ALLELES OF THE HUMAN MU OPIOID RECEPTOR, DIAGNOSTIC
; TITLE OF INVENTION: METHODS OF USING SAID ALLELES, AND METHODS OF TREATMENT
; TITLE OF INVENTION: BASED THEREON
; FILE REFERENCE: 600-1-226N
; CURRENT APPLICATION NUMBER: US/09/351,198
; CURRENT FILING DATE: 1999-07-09
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; EARLIER APPLICATION NUMBER: 60/092,402
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2162
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2063)
; OTHER INFORMATION: No. 6335168feature for this position in GeneBank.
; NAME/KEY: misc_feature
; LOCATION: (2091)
; OTHER INFORMATION: No. 6337207feature for this position in GeneBank.
US-09-351-198-1

Query Match          97.7%; Score 69.4; DB 4; Length 2162;
Best Local Similarity 98.6%; Pred. No. 1.7e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCACCTGTGCCAGCCATGCGTCCGAACCGCAGCAGCCTGCGGCGGAGAGACAGCCTGT 60
    |||||||
DB 328 GCACCTGTGCCAGCCATGCGTCCGAACCGCAGCAGCAGCCTGT 387

QY 61 GCCCTCCGACC 71
    |||||||
DB 388 GCCCTCCGACC 398

RESULT 5
US-09-113-426-1
; Sequence 1, Application US/09113426
; Patent No. 6337207
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary J
; APPLICANT: Laforge, Karl S
; APPLICANT: Yu, Lei
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: ALLELES OF THE HUMAN MU OPIOID RECEPTOR, DIAGNOSTIC
; TITLE OF INVENTION: METHODS OF USING SAID ALLELES, AND METHODS OF TREATMENT
; TITLE OF INVENTION: BASED THEREON
; FILE REFERENCE: 600-1-226
; CURRENT APPLICATION NUMBER: US/09/113,426
; CURRENT FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2162
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2063)
; OTHER INFORMATION: No. 6337207feature for this position in GeneBank.
; NAME/KEY: misc_feature
; LOCATION: (2091)
; OTHER INFORMATION: No. 6337207feature for this position in GeneBank.
US-09-113-426-1

Query Match          97.7%; Score 69.4; DB 4; Length 2162;
Best Local Similarity 98.6%; Pred. No. 1.7e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCACCTGTGCCAGCCATGCGTCCGAACCGCAGCAGCCTGCGGCGGAGAGACAGCCTGT 60
    |||||||
DB 328 GCACCTGTGCCAGCCATGCGTCCGAACCGCAGCAGCAGCCTGT 387

QY 61 GCCCTCCGACC 71
    |||||||
DB 388 GCCCTCCGACC 398
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RESULT 6  
US-08-889-108-1  
; Sequence 1, Application US/08889108  
; Patent No. 6103492  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Lei  
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/889,108  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/305,518  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: INDA005\WIM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512-418-3000  
; TELEFAX: 512-474-7577  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1618 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (cDNA)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 214..1410  
US-08-889-108-1  
  
Query Match 79.7%; Score 56.6; DB 3; Length 1618;  
Best Local Similarity 87.3%; Pred. No. 1.7e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
QY 1 GCAACCTGTCGACCCATGGGTCCGAACCGACGACTGGGGGAGAGACGCTGT 60  
Db 323 GCAACGAGTCGATCCATGGGTCTGAACCGACCGGCTTGGGGAGACGACGCTGT 382  
QY 61 GCCCTCCGACC 71  
Db 383 GCCCTCAGACC 393  
  
RESULT 7  
US-08-889-108-3  
; Sequence 3, Application US/08889108  
; Patent No. 6103492  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Lei  
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston

STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/889,108  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/305,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: INDA005\WIM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-418-3000  
TELEFAX: 512-474-7577  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1618 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (cDNA)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 339..1235  
US-08-889-108-3  
  
Query Match 79.7%; Score 56.6; DB 3; Length 1618;  
Best Local Similarity 87.3%; Pred. No. 1.7e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
QY 1 GCAACCTGTCGACCCATGGGTCCGAACCGACGACTGGGGGAGAGACGCTGT 60  
Db 323 GCAACGAGTCGATCCATGGGTCTGAACCGACCGGCTTGGGGAGACGACGCTGT 382  
QY 61 GCCCTCCGACC 71  
Db 383 GCCCTCAGACC 393  
  
RESULT 8  
US-08-120-601B-1  
; Sequence 1, Application US/08120601B  
; Patent No. 6235496  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Lei  
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/120,601B  
; FILING DATE: 13-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:



NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: INDA:002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1618 base pairs  
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STRANDEDNESS: single  
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US-08-120-601B-1

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OY 61 GCCCTCCGACC 71  
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DB 383 GCCCTCAGACC 393

RESULT 9  
US-08-120-601B-3

Sequence 3, Application US/08120601B  
Patent No. 6235496  
GENERAL INFORMATION:  
APPLICANT: Yu, Lei  
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/120.601B  
FILING DATE: 13-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: INDA:002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1618 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 339..1232  
US-08-120-601B-3

Query Match 79.7% Score 56.6; DB 4; Length 1618;  
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OY 1 GCAACCTGTCGACCCATCGGTCCGACCGACGACCTGGCGGAGAGACAGCCTGT 60  
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DB 323 GCAACGATCGCATCGGTCTGAACCGACCGGCTTGCGGAGACAGACGCTGT 382  
OY 61 GCCCTCCGACC 71  
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DB 383 GCCCTCAGACC 393

RESULT 10  
PCT-US94-10358-1

Sequence 1, Application PC/TUS9410358  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PATENT RELEASE #1.0, VERSION #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10358  
FILING DATE: Concurrently herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/120 601  
FILING DATE: 13 SEPTEMBER 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARK B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: INDA005P--  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
FILING DATE: 79-0924  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1618 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 214..1410  
PCT-US94-10358-1

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DB 323 GCAACGATCGCATCGGTCTGAACCGACCGGCTTGCGGAGACAGACGCTGT 382  
OY 61 GCCCTCCGACC 71  
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RESULT 11

PCT-US94-10358-3  
Sequence 3, Application PC/TUS9410358  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10358  
FILING DATE: Concurrently herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/120,601  
FILING DATE: 13 SEPTEMBER 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARK B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: IND0005P--  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ. ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1618 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 339..1235  
PCT-US94-10358-3

Query Match 79.7%; Score 56.6; DB 5; Length 1618;  
Best Local Similarity 87.3%; Pred. No. 1.7e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCAACTGTCCGACCATGCGGTCCGAACCGACCGACTGGGCGGAGAGACAGCCTGT 60  
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DB 323 GCAACGATCCGATCGATCGGTCTGAACCGACCGGCGCTTGGCGGGAACGACAGCCTGT 382  
QY 61 GCCCTCGACC 71  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 383 GCCCTCGACC 393

RESULT 12  
US-08-430-286A-1  
Sequence 1, Application US/08430286A  
Patent No. 6225080  
GENERAL INFORMATION:  
APPLICANT: Uhl, George R.  
APPLICANT: Epler, C. Mark  
APPLICANT: Wang, Jai-Bel  
TITLE OF INVENTION: Mu-Subtype Opioid Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York

COUNTRY: US  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,286A  
FILING DATE: 28-APR-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: RODINSON, Joseph R.  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 0646/1A843-US5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2135 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
IMMEDIATE SOURCE:  
CLONE: mu receptor cDNA  
US-08-430-286A-1

Query Match 79.7%; Score 56.6; DB 4; Length 2135;  
Best Local Similarity 87.3%; Pred. No. 1.7e-09;  
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 GCAACTGTCCGACCATGCGGTCCGAACCGACCGACTGGGCGGAGAGACAGCCTGT 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 140 GCAACGATCCGATCGATCGGTCTGAACCGACCGGCGCTTGGCGGGAACGACAGCCTGT 199  
QY 61 GCCCTCGACC 71  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 200 GCCCTCGACC 210

RESULT 13  
US-08-387-707-15  
Sequence 15, Application US/08387707  
Patent No. 6265563  
GENERAL INFORMATION:  
APPLICANT: EVANS, CHRISTOPHER J.  
APPLICANT: KEITH, DUANE E.  
TITLE OF INVENTION: OPIOID RECEPTOR GENES  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,707  
FILING DATE: 10-SEP-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: MORASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959

```

: REFERENCE/DOCKET NUMBER: 22000-20526. 20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1981 base pairs
: TYPE: nucleic acid
: STRADEDNESS: single
: TOPOLOGY: linear
: US-08-387-707-15

Query Match      75.2%: Score 53.4; DB 4; Length 1981:
Best Local Similarity 84.5%: Pred. No. 1.7e+08;
Matches 60; Conservative 0; Mismatches 11; Indels 0; Gaps 0.

QY      1  GCAACCTGTCCGACCCATCGCGTCCGAACCGCACCGACCTGGCGGAGAGACAGCCTGT 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      365  GAAACCAATCCGACCCATCGCGTCTCTAACCGAGCGGCGCTTGGCGGAAACGACAGCCTGT 424
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      61  GCCCTCGCACC 71
      ||||| |||||
Db      425  GCCCTCGACACC 435

RESULT 14
US-09-171-461-29
: Sequence 29, Application US/09171461
: Patent No. 6335016
: GENERAL INFORMATION:
: APPLICANT: Baker, Adam
: APPLICANT: Cotten, Matthew
: APPLICANT: ChioCCA, Susanna
: APPLICANT: Kutzbauer, Robert
: APPLICANT: Schaffner, Gotthold
: TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
: FILE REFERENCE: 0652.1800000
: CURRENT APPLICATION NUMBER: US/09/171,461
: CURRENT FILING DATE: 1999-01-12
: EARLIER APPLICATION NUMBER: PCT/EP97/01944
: EARLIER FILING DATE: 1997-04-18
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 29
: LENGTH: 1728
: TYPE: DNA
: ORGANISM: CELO VIRUS
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1728)
: US-09-171-461-29

Query Match      34.1%: Score 24.2; DB 4; Length 1728:
Best Local Similarity 62.3%: Pred. No. 21;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0.

QY      2  CAACCTGTCCGACCCATCGCGTCCGAACCGCACCGACCTGGCGGAGAGACAGCCTGTG 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      801  CACCTGTCCGAGCGCGGGGTAAACCGACCGACCGCGGCTGCCCTTAAGAGACCGCACCG 860
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      62  C 62
      |
Db      861  C 861

RESULT 15
US-09-171-461-1/C
: Sequence 1, Application US/09171461
: Patent No. 6335016
: GENERAL INFORMATION:
: APPLICANT: Baker, Adam
: APPLICANT: Cotten, Matthew
: APPLICANT: ChioCCA, Susanna

```

```

APPLICANT: Kurzbaner, Robert
APPLICANT: Schaffner, Gotthold
TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
FILE REFERENCE: 0652.1800000
CURRENT APPLICATION NUMBER: US/09/171,461
CURRENT FILING DATE: 1999-01-12
EARLIER APPLICATION NUMBER: PCT/EP97/01944
EARLIER FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 43804
TYPE: DNA
ORGANISM: CELO Virus
FEATURE:
NAME/KEY: gene
LOCATION: (12193)..(15043)
OTHER INFORMATION: /gene: L1
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15080)
OTHER INFORMATION: /note= L2 region penton base splice acceptor site
FEATURE:
NAME/KEY: gene
LOCATION: (15110)..(17495)
OTHER INFORMATION: /gene: L2
FEATURE:
NAME/KEY: polyA_site
LOCATION: (17526)
FEATURE:
NAME/KEY: gene
LOCATION: (17559)..(21754)
OTHER INFORMATION: /gene: L3
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18261)
OTHER INFORMATION: /gene: L3 /note= hexon splice acceptor site
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21102)
OTHER INFORMATION: /gene: L3 /note= protease splice acceptor site
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21123)
OTHER INFORMATION: /gene: L3 /note= protease splice acceptor site
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21767)
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21824)
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21836)
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21882)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (23608)
OTHER INFORMATION: /note= 100K splice acceptor site
FEATURE:
NAME/KEY: misc_feature
LOCATION: (23649)
OTHER INFORMATION: /note= 100K splice acceptor site
FEATURE:
NAME/KEY: gene
LOCATION: (23680)..(27886)
OTHER INFORMATION: /gene: L4
FEATURE:
NAME/KEY: polyA_site
LOCATION: (27920)
FEATURE:

```

NAME/KEY: misc\_feature  
LOCATION: (28315)  
OTHER INFORMATION: /note= fibre splice acceptor site  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (28341)  
OTHER INFORMATION: /note= fibre splice acceptor site  
FEATURE:  
NAME/KEY: gene  
LOCATION: (28363)..(31768)  
OTHER INFORMATION: /gene: L5  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (30511)  
OTHER INFORMATION: /gene: L5 /note= fibre splice acceptor site  
FEATURE:  
NAME/KEY: polyA\_site  
LOCATION: (31770)  
US-09-171-461-1

Query Match  
Best Local Similarity 34.1%; Score 24.2; DB 4; Length 43804;  
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2 CAACCTGTCCGACCCATGCGGTCCGAACCGCACCGACCTGGCGGAGAGACAGCCTGTG 61  
Db 11196 CACCCTGTGAGCGCGGCGGTAAACCGCACCGACCGCCTGCGCCCTAGAGACCGCACG 11137

OY 62 C 62  
Db 11136 C 11136

RESULT 16  
US-08-727-688-1  
Sequence 1, Application US/08727688  
Patent No. 5919638  
GENERAL INFORMATION:  
APPLICANT: Russell, John C.  
TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road D377/AP6D  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/727,688  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Poremski, Priscilla E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5967.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (847) 937-0378  
TELEFAX: (847) 938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 367 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
US-08-727-688-1

Query Match  
Best Local Similarity 33.8%; Score 24; DB 2; Length 367;  
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGCACCGACCTGGCGGAGAGACAGCCTGT 60  
Db 107 GCAACGAGTGGACCTAGTGGCTCTCACTGCTTCCCTGCGGCGTGGCGCTGCCGCTGA 166

OY 61 GCCC 64  
Db 167 CCC 170

RESULT 17  
US-08-727-688-9  
Sequence 9, Application US/08727688  
Patent No. 5919638

GENERAL INFORMATION:  
APPLICANT: Russell, John C.  
TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road D377/AP6D  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/727,688

FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Poremski, Priscilla E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5967.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (847) 937-0378  
TELEFAX: (847) 938-2623  
TELEX:

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1297 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-727-688-9

Query Match  
Best Local Similarity 33.8%; Score 24; DB 2; Length 1297;  
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGCACCGACCTGGCGGAGAGACAGCCTGT 60  
Db 107 GCAACGAGTGGACCTAGTGGCTCTCACTGCTTCCCTGCGGCGTGGCGCTGCCGCTGA 166

OY 61 GCCC 64  
Db 167 CCC 170

RESULT 18

US-09-020-956-109  
; Sequence 109, Application US/09020956  
; Patent No. 6261562  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/020,956  
; FILING DATE: 09-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1524 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-09-020-956-109  
Query Match 33.8%; Score 24; DB 4; Length 1524;  
Best Local Similarity 60.9%; Pred. No. 24;  
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 1 GCAACCTGCCAGCCATCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60  
DB 116 GGAACGAGTGCAGCCTAGTGGCTTCACCTGCTCTCCTGGGCGTGGGCTGCCGCTGA 175  
QY 61 GCCC 64  
DB 176 CCCC 179  
RESULT 19  
US-09-030-607-109  
; Sequence 109, Application US/09030607  
; Patent No. 6262245  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
; NUMBER OF SEQUENCES: 224  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,607  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.427C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 109:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1524 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-030-607-109  
Query Match 33.8%; Score 24; DB 4; Length 1524;  
Best Local Similarity 60.9%; Pred. No. 24;  
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 1 GCAACCTGCCAGCCATCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60  
DB 116 GGAACGAGTGCAGCCTAGTGGCTTCACCTGCTCTCCTGGGCGTGGGCTGCCGCTGA 175  
QY 61 GCCC 64  
DB 176 CCCC 179  
RESULT 20  
US-09-439-313-109  
; Sequence 109, Application US/09439313  
; Patent No. 6329505  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yugu  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retler, Mark  
; APPLICANT: Solk, John  
; APPLICANT: Day, Craig  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; FILE REFERENCE: 210121.427C9  
; CURRENT APPLICATION NUMBER: US/09/439,313  
; CURRENT FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 575  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 109  
; LENGTH: 1524  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-439-313-109  
Query Match 33.8%; Score 24; DB 4; Length 1524;  
Best Local Similarity 60.9%; Pred. No. 24;  
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 1 GCAACCTGCCAGCCATCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60  
DB 116 GGAACGAGTGCAGCCTAGTGGCTTCACCTGCTCTCCTGGGCGTGGGCTGCCGCTGA 175



```

; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-404-650-1

Query Match
Best Local Similarity 32.7%; Score 23.2; DB 4; Length 6816;
Matches 40; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 1 GCAACCTGTCGACCCATGCGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6517 GCAGCCTGCCCCCCCCCGCCGCCGCCGCCGCCGCCGCCCTGGCCACAGGCTGGCCGGA 6576

QY 61 GCCCTCCG 68
    ||| |||
Db 6577 GCCCTCCG 6584

RESULT 25
US-09-404-650-3
; Sequence 3, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McIver, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-404-650-3

Query Match
Best Local Similarity 32.7%; Score 23.2; DB 4; Length 6855;
Matches 40; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCCATGCGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6556 GCAGCCTGCCCCCCCCCGCCGCCGCCGCCGCCGCCGCCCTGGCCACAGGCTGGCCGGA 6615

QY 61 GCCCTCCG 68
    ||| |||
Db 6616 GCCCTCCG 6623

RESULT 26
US-09-030-607-195/C
; Sequence 195, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-030-607-195

Query Match
Best Local Similarity 32.4%; Score 23; DB 4; Length 502;
Matches 38; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

QY 7 TGTCCGACCCATGCGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGTGCTTC 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 TGTGTGATCCAGACTCAGGAGCTCTTCTCTGTGGGGGACACAGACCCCTTCCCTT 219

QY 67 CGACC 71
    || ||
Db 218 CCTCC 214

RESULT 27
US-09-439-313-195/C
; Sequence 195, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 195
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
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NAME/KEY: CDS  
LOCATION: 303..1334  
US-08-590-563-1

Query Match 32.4%; Score 23; DB 4; Length 1375;  
Best Local Similarity 57.7%; Pred. No. 48;  
Matches 41; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY 1 GGAACCTGTCGACCCATCGGTCGCAACCGACCGACTGGCGGAGAGACAGCTGT 60  
DB 886 GGAACCACTTGGAGCTGGCGCGCGGCGATGACCTGGCGAGCCAGCACTACCA 945  
OY 61 GCCCTCCGACC 71  
DB 946 TCATGCCGACC 956

## RESULT 30

PCT-US91-06532-1

Sequence 1, Application PC/TUS9106532

GENERAL INFORMATION:

APPLICANT: Roizman, Bernard

TITLE OF INVENTION: Recombinant Herpes Simplex Viruses

TITLE OF INVENTION: Vaccines and Methods

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp;

ADDRESSER: Bicknell

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/06532

FILING DATE: 19910910

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Gruber, Lewis S.

REGISTRATION NUMBER: 30,060

REFERENCE/DOCKET NUMBER: 27373/8235

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/346-5750

TELEFAX: 312/984-9740

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1335 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US91-06532-1

Query Match 32.1%; Score 22.8; DB 5; Length 1335;

Best Local Similarity 59.1%; Pred. No. 55;

Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY 6 CTGTCCGACCCATCGGTCGCAACCGACCGACTGGCGGAGAGACAGCTGTGCT 65  
DB 428 CCGCCCCCGCGGTCGCCACCGCGCGCGGCGGCGGCGGCGGCGGCGCTAACCCCT 487

OY 66 CCGACC 71  
DB 488 CCCACC 493

RESULT 31

US-08-247-901C-1/c  
Sequence 1, Application US/08247901C  
Patent No. 5750384

GENERAL INFORMATION:

APPLICANT: Jacobs et al

TITLE OF INVENTION: L5 SHUTTLE PHASMIDS

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amster, Rothstein &amp; Ebenstein

STREET: 90 Park Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Word Processor (ASCII)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/247,901C

FILING DATE: May 23, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/057,531

FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Bogosian, Elizabeth A

REGISTRATION NUMBER: 39,911

REFERENCE/DOCKET NUMBER: 96700/273

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 697-5995

TELEFAX: (212) 286-0854 or 286-0082

TELEX: TWX 710-381-4766

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 50341

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:

DESCRIPTION: L5 shuttle phasmid sequence

HYPOTHETICAL: NO

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: L5 mycobacteriophage

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

IMMEDIATE SOURCE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION: No. 5750384e

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:  
US-08-247-901C-1

Query Match 32.1%; Score 22.8; DB 1; Length 50341;  
Best Local Similarity 59.1%; Pred. No. 73;  
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 5 CCTGTCCGACCCATGCGTCCGACCGACCTGGCGGAGAGACAGCTGTGCC 64  
Db 31163 CCAGCGCTACTGGCGGTATGAGCAGAAAGATCTGCCGAGAACTACGCGTGAACCC 31104

QY 65 TCCGAC 70  
Db 31103 TGCCAC 31098

RESULT 32  
US-09-075-904-1/C  
Sequence 1, Application US/09075904  
Patent No. 5994137  
GENERAL INFORMATION:  
APPLICANT: Jacobs, et al.  
TITLE OF INVENTION: L5 SHUTTLE PHASMIDS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amster, Rothstein & Ebnstein  
STREET: 90 Park Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Processor (ASCII)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/075,904  
FILING DATE: May 11, 1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/247,901  
FILING DATE: May 23, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bogosian, Elizabeth A  
REGISTRATION NUMBER: 39,911  
REFERENCE/DOCKET NUMBER: 96700/475  
TELEPHONE: (212) 697-5995  
TELEFAX: (212) 286-0854 or 286-0082  
TELEX: TWX 710-581-4766  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50341  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: L5 shuttle phasmid sequence  
HYPOTHETICAL: NO  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: L5 mycobacteriophage  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:

POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION: No. 5994137e  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-09-075-904-1

Query Match 32.1%; Score 22.8; DB 2; Length 50341;  
Best Local Similarity 59.1%; Pred. No. 73;  
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 5 CCTGTCCGACCCATGCGTCCGACCGACCTGGCGGAGAGACAGCTGTGCC 64  
Db 31163 CCAGCGCTACTGGCGGTATGAGCAGAAAGATCTGCCGAGAACTACGCGTGAACCC 31104

QY 65 TCCGAC 70  
Db 31103 TGCCAC 31098

RESULT 33  
US-09-426-436-1/C  
Sequence 1, Application US/09426436  
Patent No. 6225066  
GENERAL INFORMATION:  
APPLICANT: William R. Jacobs, Jr.  
APPLICANT: Barry R. Bloom  
APPLICANT: Graham F. Halfull  
TITLE OF INVENTION: MYCOBACTERIAL SPECIES-SPECIFIC  
TITLE OF INVENTION: REPORTER MYCOBACTERIOPHAGES  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amster, Rothstein & Ebnstein  
STREET: 90 Park Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Processor (ASCII)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/426,436  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/705,557  
FILING DATE:  
APPLICATION NUMBER: US/08/057,531  
FILING DATE:  
APPLICATION NUMBER: 07/833,431  
FILING DATE: February 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: 96700/238  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 697-5995

TELEFAX: (212) 286-0854 or 286-0082  
TELEX: TWX 710-581-4766  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52297  
TYPE: nucleotide  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: phage genome sequence  
HYPOTHETICAL: no  
ANTISENSE: no  
FRAGMENT TYPE: not applicable.  
ORIGINAL SOURCE:  
ORGANISM: mycobacteriophage L5  
STRAIN: not applicable  
INDIVIDUAL ISOLATE: L5  
DEVELOPMENTAL STAGE: not applicable  
HAPLOTYPE: not applicable  
TISSUE TYPE: not applicable  
CELL TYPE: not applicable  
ORGANELLE: not applicable  
IMMEDIATE SOURCE: mycobacteriophage L5 particles  
POSITION IN GENOME: entire genome  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS: Hatfull and Sarkis  
TITLE: DNA Sequence, Structure and Gene  
TITLE: Expression of Mycobacteriophage L5:  
TITLE: A Phage System for Mycobacterial  
TITLE: Genetics  
JOURNAL: Molecular Microbiology  
VOLUME: 7  
PAGES: 395-405  
DATE: 1993  
US-09-426-436-1

Query Match 32.1%; Score 22.8; DB 4; Length 52297;  
Best Local Similarity 59.1%; Pred. No. 73;  
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 5 CCTGTCCGACCATCGGTCCGACCGACCGACCTGGGGGAGAGACAGCCTGTGCC 64  
DB 31060 CCAGCGCTACTGGGCGGTATGAGCAGAAAGATCTCGCCGAGAACTACGGCGTGAACCC 31001

QY 65 TCCGAC 70  
DB 31000 TCCGAC 30995

RESULT 34  
US-08-705-557-1/C  
Sequence 1, Application US/08705557  
Patent No. 6300061  
GENERAL INFORMATION:  
APPLICANT: William R. Jacobs, Jr.  
APPLICANT: Barry R. Bloom  
APPLICANT: Graham F. Hatfull  
TITLE OF INVENTION: MYCOBACTERIAL SPECIES-SPECIFIC  
TITLE OF INVENTION: REPORTER MYCOBACTERIOPHAGES  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amster, Rothstein & Ebenstein  
STREET: 90 Park Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Processor (ASCII)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/705,557  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/057,531  
FILING DATE:  
APPLICATION NUMBER: 07/833,431  
FILING DATE: February 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasquallini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: 96700/238  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 697-5995  
TELEFAX: (212) 286-0854 or 286-0082  
TELEX: TWX 710-581-4766  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52297  
TYPE: nucleotide  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: phage genome sequence  
HYPOTHETICAL: no  
ANTISENSE: no  
FRAGMENT TYPE: not applicable.  
ORIGINAL SOURCE:  
ORGANISM: mycobacteriophage L5  
STRAIN: not applicable  
INDIVIDUAL ISOLATE: L5  
DEVELOPMENTAL STAGE: not applicable  
HAPLOTYPE: not applicable  
TISSUE TYPE: not applicable  
CELL TYPE: not applicable  
CELL LINE: not applicable  
ORGANELLE: not applicable  
IMMEDIATE SOURCE: mycobacteriophage L5 particles  
POSITION IN GENOME: entire genome  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS: Hatfull and Sarkis  
TITLE: DNA Sequence, Structure and Gene  
TITLE: Expression of Mycobacteriophage L5:  
TITLE: A Phage System for Mycobacterial  
TITLE: Genetics  
JOURNAL: Molecular Microbiology  
VOLUME: 7  
PAGES: 395-405  
DATE: 1993  
US-08-705-557-1

Query Match 32.1%; Score 22.8; DB 4; Length 52297;  
Best Local Similarity 59.1%; Pred. No. 73;  
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 5 CCTGTCCGACCATCGGTCCGACCGACCGACCTGGGGGAGAGACAGCCTGTGCC 64  
DB 31060 CCAGCGCTACTGGGCGGTATGAGCAGAAAGATCTCGCCGAGAACTACGGCGTGAACCC 31001

QY 65 TCCGAC 70  
DB 31000 TCCGAC 30995

```
RESULT 35
US-09-103-840A-2/C
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match          32.1%; Score 22.8; DB 4; Length 4403765;
Best Local Similarity 62.1%; Pred. No. 47;
Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY      2  CAACCTGTCGACCCATCGGTCCGACCGACCTGGCGGAGAGACAGCCTG 59
Db 3472436  CAACCTGTCGACCCATCGGTCCGACCGACCGACCGAGAGAGAGCAGTGTGCTG 3472379

RESULT 36
US-09-103-840A-1/C
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          32.1%; Score 22.8; DB 4; Length 4411529;
Best Local Similarity 62.1%; Pred. No. 47;
Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY      2  CAACCTGTCGACCCATCGGTCCGACCGACCTGGCGGAGAGAGACAGCCTG 59
Db 3476686  CAACCTGTCGACCCATCGGTCCGACCGACCGAGAGAGAGAGCAGTGTGCTG 3476629

RESULT 37
PCT-US93-06251-22
; Sequence 22, Application PC/TUS9306251
; GENERAL INFORMATION:
```

```
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-22

Query Match          31.8%; Score 22.6; DB 5; Length 4522;
Best Local Similarity 60.7%; Pred. No. 70;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY      11  CGACCCATGGGTCGCCGACCGACCGACCTGGCGGAGAGAGAGCCTGTGCTCCGAC 70
Db 312  CGACCCATGGTGTCCGCCGCCGCCGCCAGGTTTAAGCAGAGACTGGAACTCTCGC 371

QY      71  C 71
Db 372  C 372

RESULT 38
US-09-056-105-12
; Sequence 12, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 4736
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-12

Query Match          31.8%; Score 22.6; DB 4; Length 4736;
```



1 APPLICANT: Strathy, Nancy  
 2 APPLICANT: Fantini, Susan E.  
 3 TITLE OF INVENTION: Cloning of the biosynthetic pathway for  
 4 TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmid  
 5 TITLE OF INVENTION: useful therein  
 6 NUMBER OF SEQUENCES: 1  
 7 CORRESPONDENCE ADDRESSES:  
 8 ADDRESSEE: American Cyanamid Company  
 9 STREET: One Cyanamid Plaza  
 10 CITY: Wayne  
 11 STATE: New Jersey  
 12 COUNTRY: USA  
 13 ZIP: 07470  
 14 COMPUTER READABLE FORM:  
 15 MEDIUM TYPE: Floppy disk  
 16 COMPUTER: IBM PC compatible  
 17 OPERATING SYSTEM: PC-DOS/MS-DOS  
 18 SOFTWARE: Patentin Release #1.0, Version #1.25  
 19 CURRENT APPLICATION DATA:  
 20 APPLICATION NUMBER: US/08/474,933  
 21 FILING DATE:  
 22 CLASSIFICATION: 435  
 23 PRIOR APPLICATION DATA:  
 24 APPLICATION NUMBER: US 08/125,468  
 25 FILING DATE: 22-SEP-1993  
 26 ATTORNEY/AGENT INFORMATION:  
 27 NAME: Tsevdos, Estelle J  
 28 REGISTRATION NUMBER: 31,145  
 29 REFERENCE/DOCKET NUMBER: 31,255-02  
 30 TELECOMMUNICATION INFORMATION:  
 31 TELEPHONE: (201)831-3241  
 32 TELEFAX: (201)831-3305  
 33 INFORMATION FOR SEQ ID NO: 1:  
 34 SEQUENCE CHARACTERISTICS:  
 35 LENGTH: 30001 base pairs  
 36 TYPE: nucleic acid  
 37 STRANDEDNESS: single  
 38 TOPOLOGY: linear  
 39 MOLECULE TYPE: DNA (genomic)  
 40 US-08-474-933-1

```

Query Match          31.8%; Score 22.6; DB 2; Length 30001;
Best Local Similarity 60.7%; Pred. No. 82;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps

OY      2  CAACCTGTCGACCCATCGGCTCGACACCGCACTGGCGGGAGAGACAGCCTGTG 61
          | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 15440 CGAGGCGTCGCCGCCGGGCTCGACCAAGATCCGCCGCAACTGGCGCTCGGCAACCGCTGTT 15499

OY      62 C 62
          |
Db      15500 C 15500

RESULT 43
US-08-923-137-2/C
; Sequence 2, Application US/08923137
; Patent No. 6083716
;
GENERAL INFORMATION:
;
APPLICANT: Wilson, James M.
APPLICANT: Farina, Steven F.
APPLICANT: Fisher, Krishna J.
TITLE OF INVENTION: Chimpazee Adenovirus Vectors
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: United States of America
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

```

:
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/923,137
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/024,700
: FILING DATE: 06-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Bak, Mary E.
: REGISTRATION NUMBER: 31,215
: REFERENCE/DOCKET NUMBER: 31,215
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-540-9200
: TELEFAX: 215-540-5818
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 36519 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: CDNA
:
: US-08-923-137-2

```

	Query Match	31.8%	Score 22.6:	DB 3,	Length 36519;
	Best Local Similarity	60.7%	Pred. No. 82;		
Matches	37;	Conservative	0;	Mismatches	24; Indels 0; Gaps 0;
OY	2 CAACCTGCCAGCCGATCGGCGCAACCGCAGACGTCGGCGGAGAGACGCCTG	61			
Dd	34024 CAACCTGGTGTCTGTCTTTGTCAGCTACTGACGACCACTTGACGAGATCCGATGGCTG	33965			
OY	62 C 62				
Dd	33964 C 33964				

```

RESULT 44
US-09-105-537-5
: Sequence 5, Application US/09105537A
: Patent No. 6265202
: GENERAL INFORMATION:
: APPLICANT: Sherman, D.H.
: APPLICANT: Liu, H.
: APPLICANT: Xue, Y.
: APPLICANT: Zhao, L.
: TITLE OF INVENTION: DNA encoding methymycin and pikromycin
: FILE REFERENCE: 600.438US1
: CURRENT APPLICATION NUMBER: US/09/105,537A
: CURRENT FILING DATE: 1998-06-26
: NUMBER OF SEQ. ID NOS: 43
: SOFTWARE: fastseq for Windows Version 3.0
: SEQ. ID NO 5
: LENGTH: 36778
: TYPE: DNA
: ORGANISM: Streptomyces venezuelae
: US-09-105-537-5

```

```
Query Match      31.8%; Score 22.6; DB 4, Length 36778;  
Best Local Similarity   60.7%; Pred. No. 82;  
Matches    37; Conservative     0; Mismatches    24; Indels       0; Gaps        0.  
  
QY           1 GCACCTGTCGCACCATTGGCGTCCGAAGCAGCACGCCACTGTGTTGGCGGGAGACAGACAGCCTGT 60  
              |||||         |  |||  |||||  |||||  |||  |||||  ||  
Db          2124 GGAAAGCCCGGCGACTTCAACGACCGGAGACCGTGCGCCCCGGCGCGCTCGAACAAGCCGGT 2183  
  
QY           61 G 61  
Db          2184 G 2184
```

```
RESULT 45
US-09-320-878-19
; Sequence 19, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; EARLIER FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 19
; LENGTH: 38506
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-19

Query Match          31.8%; Score 22.6; DB 3; Length 38506;
Best Local Similarity 60.7%; Pred. No. 83;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 1 GCAACCTGTCGACCCATGGTCCGACCGCGACCGCGGCGGAGAGACGCTGT 60
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Db 266 GGAACCGCGCGCCTTCTACGACCCGCGACCGCTCGCCGCCCTCGACAGCGCGT 325
OY 61 G 61
Db 326 G 326

RESULT 46
US-09-428-517-1/C
; Sequence 1, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
; APPLICANT: Betlach, Mary C.
; APPLICANT: Shah, Sanjay Krishnakant
; APPLICANT: MCDANIEL, Robert
; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLFANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428,517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 50937
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant DNA
US-09-428-517-1
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Query Match          31.8%; Score 22.6; DB 4; Length 50937;
Best Local Similarity 60.7%; Pred. No. 84;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 10 CCGACCCATGGGTCCGACCGCGACCTGGCGGAGAGACACCTGTGCTCCGA 69
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Db 43639 CCGACGATGAGGTCCGACCCCGACAGACCGCGGTGGCGGTGCGGTGCCGCGC 43580
OY 70 C 70
Db 43579 C 43579

RESULT 47
US-09-170-331-3
; Sequence 3, Application US/09170331C
; Patent No. 6028175
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R
; APPLICANT: Grandy, David K
; TITLE OF INVENTION: A No. 6028175e1 Mammalian Methadone-Specific Opioid Receptor
; FILE REFERENCE: 93-311-C
; CURRENT APPLICATION NUMBER: US/09/170,331C
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (182)..(1282)
US-09-170-331-3

Query Match          31.5%; Score 22.4; DB 3; Length 1452;
Best Local Similarity 59.4%; Pred. No. 74;
Matches 38; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY 1 GCAACCTGTCGACCCATGGGTCCGACCGCGACCTGGCGGAGAGACGCTGT 60
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Db 240 GGAACCTGTCCTCTAATGAGACGCTACCCACCCACCTGCTCTCAATGTATGATCA 299
OY 61 GCCC 64
Db 300 GCCG 303

RESULT 48
US-08-967-101-96/C
; Sequence 96, Application US/08967101
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESLA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:32:12 : Search time 1712 Seconds  
(without alignments)  
559.745 Million cell updates/sec

Title: US-09-626-616-7\_COPY\_354\_424

Perfect score: 71

Sequence: 1 GCACCGTCGCCGACCATGC.....ACACCGTCGCCCTCCGACC 71

Scoring table:

IDENTITY\_NUC  
Gap 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27433522

Minimum DB seq length: 35

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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5	29.2	41.1	722	10	B1552111 603195053
6	28	39.4	454	12	AQ308543 CTMBI-R1-
7	27.6	38.9	605	12	FR003905
8	27.4	38.6	921	10	BF305771
9	27	38.0	848	10	BG615009
10	26.6	37.5	673	10	BF527152
11	26.6	37.5	799	10	BF541519
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13	26.6	37.5	909	12	CNS02R80
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70	25.6	36.1	769	10	BE256988
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82	25.4	35.8	614	10	BE761228
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92	25.4	35.8	1033	10	BE371962	BE371962	c 165	24.8	34.9	876	10	BF307938	BF307938	601889528
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96	25.2	35.5	407	9	BE237408	BE237408	c 169	24.8	34.9	919	10	BF304092	BF304092	601888602
97	25.2	35.5	411	9	AM252517	UI-R-BJO	c 170	24.8	34.9	927	10	BE205492	BE205492	602753349
98	25.2	35.5	469	9	BE149865	BE149865	c 171	24.8	34.9	934	10	BE205492	BE205492	601867887
99	25.2	35.5	470	10	BF656599	UI-R-BJO	c 172	24.8	34.9	939	10	BF205339	BF205339	601867912
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102	25.2	35.5	646	10	BM440748	BM440748	c 175	24.8	34.9	1004	10	BF308958	BF308958	601889628
103	25.2	35.5	669	12	AG137616	AG137616	c 176	24.8	34.9	1058	10	BC177741	BC177741	602314920
104	25.2	35.5	979	12	CNS0142X	AL103635	c 177	24.8	34.6	2630	11	AP318382	AP318382	AT2EC20TF
105	25.2	35.5	106	12	BH229623	Drosophila	c 178	24.6	34.6	103	12	BH244449	BH244449	BM173359
106	25.2	35.5	137	12	BH232344	BH232344	c 179	24.6	34.6	186	12	BH173359	BH173359	0104A10 m
107	25.2	35.2	291	9	AJ397894	AJ397894	c 180	24.6	34.6	277	12	AO937823	AO937823	NB6-534R
108	25.2	35.2	449	9	AI014939	AI014939	c 181	24.6	34.6	295	10	BM147612	BM147612	TCAP1013
109	25.2	35.2	487	10	BF276699	BF276699	c 182	24.6	34.6	379	10	BI535496	BI535496	MA
110	25.2	35.2	579	10	AA976022	AA976022	c 183	24.6	34.6	428	10	BM194036	BM194036	MA
111	25.2	35.2	681	12	CNS02FE9	AL194922	c 184	24.6	34.6	429	9	AI951245	AI951245	wk65D02.x
112	25.2	35.2	704	12	AG114921	AG114921	c 185	24.6	34.6	479	10	BI680573	BI680573	458878 MA
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115	25.2	35.2	884	10	BM051415	BM051415	c 188	24.6	34.6	520	10	BE479927	BE479927	164797 BA
116	25.2	35.2	994	12	CNS026JL	BM051415	c 189	24.6	34.6	520	10	BE684502	BE684502	185907 MA
117	25.2	35.2	245	9	AI192263	AI192263	c 190	24.6	34.6	522	12	AO593554	AO593554	HS_5462_A
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125	24.8	34.9	445	9	AI366197	AI366197	c 198	24.6	34.6	765	12	AC163294	AC163294	MA
126	24.8	34.9	446	9	AI366226	AI366226	c 199	24.6	34.6	789	10	BC286805	BC286805	602382664
127	24.8	34.9	451	10	BM055068	BM055068	c 200	24.6	34.6	848	10	BI197732	BI197732	602757664
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130	24.8	34.9	462	9	AI365657	AI365657	c 203	24.6	34.6	1096	12	CNS014521	CNS014521	Drosophila
131	24.8	34.9	466	10	BC626810	BC626810	c 204	24.6	34.6	1135	12	CNS04421	CNS04421	MA
132	24.8	34.9	472	10	BF987261	BF987261	c 205	24.4	34.4	227	9	BB350173	BB350173	Tetraodon
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137	24.8	34.9	568	10	BF920370	BF920370	c 210	24.4	34.4	476	10	BE950518	BE950518	QVO-GN014
138	24.8	34.9	584	10	BC003082	BC003082	c 211	24.4	34.4	503	10	BM484872	BM484872	538877 MA
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145	24.8	34.9	678	10	BF317304	BF317304	c 218	24.4	34.4	1033	10	BF111151	BF111151	601898617
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147	24.8	34.9	711	10	BI113825	BI113825	c 220	24.4	34.4	1414	10	BF122001	BF122001	601756343
148	24.8	34.9	718	10	BE313402	BE313402	c 221	24.2	34.1	380	9	BB871023	BB871023	MA
149	24.8	34.9	752	9	AL548785	AL548785	c 222	24.2	34.1	443	10	BF346172	BF346172	602017638
150	24.8	34.9	752	10	BF791571	BF791571	c 223	24.2	34.1	448	10	BI514870	BI514870	BM160016B
151	24.8	34.9	764	10	BM005993	BM005993	c 224	24.2	34.1	483	9	AW761747	AW761747	uq23604.Y
152	24.8	34.9	766	10	BF205817	BF205817	c 225	24.2	34.1	493	9	AA057677	AA057677	2194A03.S
153	24.8	34.9	773	10	BE295022	BE295022	c 226	24.2	34.1	501	9	BE163519	BE163519	QV3-HT046
154	24.8	34.9	780	10	BI198769	BI198769	c 227	24.2	34.1	526	10	BI460241	BI460241	6030201859
155	24.8	34.9	785	10	BM041292	BM041292	c 228	24.2	34.1	546	9	BB768843	BB768843	MA
156	24.8	34.9	803	10	BC105815	BC105815	c 229	24.2	34.1	549	12	TA99A040	TA99A040	MA
157	24.8	34.9	814	10	BF204977	BF204977	c 230	24.2	34.1	553	9	AI284197	AI284197	q126609.x
158	24.8	34.9	815	10	BM006206	BM006206	c 231	24.2	34.1	562	10	BC424878	BC424878	602453134
159	24.8	34.9	818	9	AL552519	AL552519	c 232	24.2	34.1	608	10	BI727877	BI727877	1031059C1
160	24.8	34.9	825	10	BF310007	BF310007	c 233	24.2	34.1	623	9	AW822655	AW822655	uq14605.Y
161	24.8	34.9	829	10	AL564758	AL564758	c 234	24.2	34.1	626	10	BI523151	BI523151	603175920
162	24.8	34.9	830	10	BF308466	BF308466	c 235	24.2	34.1	627	10	BB612564	BB612564	MA
163	24.8	34.9	855	9	AL552629	AL552629	c 236	24.2	34.1	639	9	BB656038	BB656038	MA

C 237	24.2	34.1	674	10	Bi724703	Bi724703 1031074D0	C 310	23.8	33.5	608	12	FR0032411	AL028779 Fugu rubr
C 238	24.2	34.1	691	10	BG548534	BG548534 602576527	C 311	23.8	33.5	618	10	BM104431	BM104431 f474003.Y
C 239	24.2	34.1	764	10	BF859532	BF859532 963002G10	C 312	23.8	33.5	628	10	BG704121	BG704121 602687301
C 240	24.2	34.1	782	10	BF312229	BF312229 601898736	C 313	23.8	33.5	648	9	BB655482	BB655482 BB655482
C 241	24.2	34.1	794	10	BF960993	BF960993 602310172	C 314	23.8	33.5	651	10	Bi997623	Bi997623 1031050H0
C 242	24.2	34.1	804	10	BF982515	BF982515 602308111	C 315	23.8	33.5	658	9	AM618939	AM618939 ESTPMC357
C 243	24.2	34.1	813	10	Bi184990	Bi184990 UNL-P-FN-	C 316	23.8	33.5	667	12	AG106821	AG106821 Pan trogl
C 244	24.2	34.1	839	10	BE378841	BE378841 601237368	C 317	23.8	33.5	679	9	BB636642	BB636642 BB636642
C 245	24.2	34.1	861	9	AL527229	AL527229 AL527229	C 318	23.8	33.5	685	10	BG743036	BG743036 602632158
C 246	24.2	34.1	861	9	AL555455	AL555455 AL555455	C 319	23.8	33.5	724	9	AM600757	AM600757 ESTPMC281
C 247	24.2	34.1	887	9	AL522765	AL522765 AL522765	C 320	23.8	33.5	731	9	AL1378265	AL1378265 tC43f01.x
C 248	24.2	34.1	924	10	Bi196179	Bi196179 6027534805	C 321	23.8	33.5	737	10	BF306187	BF306187 601893037
C 249	24.2	34.1	953	9	AL513561	AL513561 AL513561	C 322	23.8	33.5	779	10	BG475619	BG475619 602491836
C 250	24.2	34.1	959	10	BF300870	BF300870 602028870	C 323	23.8	33.5	799	12	AO865371	AO865371 nbe000254
C 251	24.2	34.1	992	12	CNS01UFO	AL167733 Tetraodon	C 324	23.8	33.5	800	12	AO865371	AO865371 nbe000254
C 252	24.2	34.1	1022	9	AL543353	AL543353 AL543353	C 325	23.8	33.5	885	12	CNS02EBL	AL193458 Tetraodon
C 253	24.2	34.1	1037	12	CNS04IVR	AL192752 Tetraodon	C 326	23.8	33.5	921	10	BG421280	BG421280 602451776
C 254	24.2	34.1	1095	12	AG077756	AG077756 Pan trogl	C 327	23.8	33.5	928	10	BE914383	BE914383 601669355
C 255	24.2	34.1	1211	10	BG619545	BG619545 602618935	C 328	23.8	33.5	931	9	AM600735	AM600735 ESTPMC226
C 256	24.2	34.1	1510	12	AG029261	AG029261 Pan trogl	C 329	23.8	33.5	1051	10	BE5562161	BE5562161 601346296
C 257	24	33.8	155	9	AA369171	AA369171 ESTR0540	C 330	23.8	33.5	1060	10	BE573591	BE573591 601333620
C 258	24	33.8	202	9	AA327303	AA327303 ESTR0615	C 331	23.8	33.5	1083	10	BF526881	BF526881 602070446
C 259	24	33.8	264	12	BH222890	BH222890 1006109G0	C 332	23.8	33.5	1130	10	Bi117761	Bi117761 602866966
C 260	24	33.8	294	12	AO994629	AO994629 RPCI-23-2	C 333	23.8	33.5	1204	10	BF203286	BF203286 601866075
C 261	24	33.8	296	10	T29281	T29281 EST74974 Hu	C 334	23.8	33.5	1430	10	BG855959	BG855959 1024044C0
C 262	24	33.8	321	9	AI916166	AI916166 wI47f02.x	C 335	23.8	33.5	3141	11	BC0133227	BC0133227 Mns muscu
C 263	24	33.8	337	10	BG252938	BG252938 602365539	C 336	23.6	33.2	139	9	AM416334	AM416334 51573 MAR
C 264	24	33.8	343	9	AA792745	AA792745 vS89d11.r	C 337	23.6	33.2	139	9	AM416335	AM416335 51574 MAR
C 265	24	33.8	363	10	C02794	C02794 C02794 Huma	C 338	23.6	33.2	162	12	A2342926	A2342926 IM0076111
C 266	24	33.8	364	9	AA336217	AA336217 EST70761	C 339	23.6	33.2	171	9	AM839909	AM839909 MR4-LTRO07
C 267	24	33.8	385	10	WA2402	WA2402 mc76e05.r1	C 340	23.6	33.2	212	10	R25625	R25625 yH45g02.r1
C 268	24	33.8	387	10	BE137064	BE137064 uG59c09.x	C 341	23.6	33.2	225	10	BB495146	BB495146 BB495146
C 269	24	33.8	390	9	AL588333	AL588333 tG66h02.x	C 342	23.6	33.2	232	9	AA225661	AA225661 nC08c11.r
C 270	24	33.8	410	10	HI8835	HI8835 yM45d10.r1	C 343	23.6	33.2	243	10	Bi402715	Bi402715 M1-P-CPI-
C 271	24	33.8	413	12	AO973857	AO973857 RPCI-23-3	C 344	23.6	33.2	243	10	R21492	R21492 yG06e09.r1
C 272	24	33.8	418	10	BM482353	BM482353 535214 MA	C 345	23.6	33.2	292	9	AV017865	AV017865 AV017865
C 273	24	33.8	442	10	N34668	N34668 yL15e07.s1	C 346	23.6	33.2	292	9	Bi173632	Bi173632 BB173632
C 274	24	33.8	444	9	AM816479	AM816479 OVO-ST023	C 347	23.6	33.2	315	9	BB255729	BB255729 BB255729
C 275	24	33.8	452	9	AA463023	AA463023 vG85b01.r	C 348	23.6	33.2	344	10	Bi184098	Bi184098 UNL-P-FN-
C 276	24	33.8	452	12	AO936675	AO936675 JNB-023R	C 349	23.6	33.2	344	10	Bi184719	Bi184719 UNL-P-FN-
C 277	24	33.8	471	10	Bi808191	Bi808191 C004D04 O	C 350	23.6	33.2	355	10	T70189	T70189 yC18c11.s1
C 278	24	33.8	475	10	BM253153	BM253153 512525 MA	C 351	23.6	33.2	371	10	BM376850	BM376850 EBem05_5Q
C 279	24	33.8	477	12	AL1754179	AL1754179 cr21d06.x	C 352	23.6	33.2	390	9	AJ280987	AJ280987 4A3A-ABA-
C 280	24	33.8	544	9	BB754536	BB754536 SALR.0305	C 353	23.6	33.2	392	9	AA394294	AA394294 zt16g05.r
C 281	24	33.8	544	9	AL1427258	AL1427258 mc76e05.y	C 354	23.6	33.2	393	10	W39779	W39779 zC80g04.r1
C 282	24	33.8	574	10	BG474234	BG474234 602516854	C 355	23.6	33.2	400	10	BE605229	BE605229 WHE1701-1
C 283	24	33.8	586	10	BG928724	BG928724 HNC72-1-C	C 356	23.6	33.2	413	9	AJ281717	AJ281717 4A3A-AAR-
C 284	24	33.8	609	9	AI911818	AI911818 wC86903.x	C 357	23.6	33.2	425	10	BF706203	BF706203 280575 MA
C 285	24	33.8	609	12	AG130993	AG130993 Pan trogl	C 358	23.6	33.2	443	10	BF327484	BF327484 OVA-BN009
C 286	24	33.8	620	12	AM851731	AM851731 MR2-CT022	C 359	23.6	33.2	445	9	AA313759	AA313759 EST183407
C 287	24	33.8	672	10	Bi759746	Bi759746 603045620	C 360	23.6	33.2	449	10	BF514268	BF514268 UT-H-BM1-
C 288	24	33.8	694	10	BE372473	BE372473 601223918	C 361	23.6	33.2	453	9	BB773282	BB773282 BB773282
C 289	24	33.8	694	12	AG114683	AG114683 Pan trogl	C 362	23.6	33.2	462	10	BF189037	BF189037 234294 MA
C 290	24	33.8	745	9	AI996994	AI996994 701551562	C 363	23.6	33.2	464	9	AJ282617	AJ282617 4A3A-ABA-
C 291	24	33.8	746	10	BE883638	BE883638 601507317	C 364	23.6	33.2	470	10	BF405458	BF405458 UT-R-Hum1
C 292	24	33.8	845	9	AL533517	AL533517 AL533517	C 365	23.6	33.2	479	10	C03257	C03257 C03257
C 293	24	33.8	845	9	AL576856	AL576856 AL576856	C 366	23.6	33.2	488	12	CNS01SAB	AL164972 Tetraodon
C 294	24	33.8	891	10	BF131004	BF131004 601820049	C 367	23.6	33.2	497	10	BF118093	BF118093 ut11907.y
C 295	24	33.8	900	10	BF981740	BF981740 6020306096	C 368	23.6	33.2	499	12	AO397939	AO397939 mGxB0007C
C 296	24	33.8	975	10	BF302143	BF302143 602033093	C 369	23.6	33.2	500	9	AV393411	AV393411 AV393411
C 297	24	33.8	1463	10	BM472176	BM472176 AGENCOURT	C 370	23.6	33.2	525	12	CNS03NEM	AL251959 Tetraodon
C 298	24	33.8	256	10	BF336269	BF336269 KC2-CT050	C 371	23.6	33.2	530	10	BF160375	BF160375 387255 MA
C 299	23.8	33.5	361	12	AO635033	AO635033 RPCI-11-4	C 372	23.6	33.2	530	10	BF394554	BF394554 UT-R-CA0-
C 300	23.8	33.5	407	9	AV760910	AV760910 AV760910	C 373	23.6	33.2	545	10	BE645586	BE645586 7672f05.x
C 301	23.8	33.5	431	9	AV429944	AV429944 A1336203 a087f09.x	C 374	23.6	33.2	577	9	AM851713	AM851713 MR2-CT022
C 302	23.8	33.5	443	9	AL366203	AL366203 a087f09.x	C 375	23.6	33.2	606	12	A2378787	A2378787 IM0133009
C 303	23.8	33.5	455	12	AO865840	AO865840 nbe00026M	C 376	23.6	33.2	609	12	A2104313	A2104313 RPCI-23-4
C 304	23.8	33.5	507	9	AV431515	AV431515 AV431515	C 377	23.6	33.2	613	9	AM180918	AM180918 MGA0036r
C 305	23.8	33.5	513	9	AV431804	AV431804 AV431804	C 378	23.6	33.2	613	9	AM745961	AM745961 W61-38-A1
C 306	23.8	33.5	520	9	AV434158	AV434158 AV434158	C 379	23.6	33.2	614	9	AV721387	AV721387 AV721387
C 307	23.8	33.5	532	9	AV434812	AV434812 AV434812	C 380	23.6	33.2	618	12	CNS02082	AL199883 Tetraodon
C 308	23.8	33.5	590	12	CNS027C4	AL21989 Tetraodon	C 381	23.6	33.2	626	9	AM851676	AM851676 MR2-CT022
C 309	23.8	33.5					C 382	23.6	33.2				

C 383	23.6	33.2	632	9	AW949652	AW949652 EST361722	456	23.4	33.0	377	9	AA652181	AA652181 ns57e02.s
C 384	23.6	33.2	636	10	BI400787	BI400787 MI-P-AVI-	C 457	23.4	33.0	377	9	AA577960	AA577960 n12aC07.s
C 385	23.6	33.2	638	12	AZ396468	AZ396468 IM0161101	C 458	23.4	33.0	377	10	BI042734	BI042734 CM4-OT016
C 386	23.6	33.2	642	9	BB549917	BB549917 BB549917	C 459	23.4	33.0	378	10	BE938422	BE938422 RCO-TN007
C 387	23.6	33.2	650	10	BM015362	BM015362 603641525	C 460	23.4	33.0	380	9	AI161323	AI161323 qb66g07.x
C 388	23.6	33.2	653	10	BI157799	BI157799 602823127	C 461	23.4	33.0	383	9	AI888548	AI888548 wn21g04.x
C 389	23.6	33.2	656	9	BB539838	BB539838 BB539838	C 462	23.4	33.0	385	9	AI810886	AI810886 lu21c12.x
C 390	23.6	33.2	663	10	BI662543	BI662543 603305351	C 463	23.4	33.0	386	9	AA335066	AA335066 EST39445
C 391	23.6	33.2	672	10	BI661031	BI661031 603304339	C 464	23.4	33.0	386	10	BE938445	BE938445 RCO-TN007
C 392	23.6	33.2	677	10	BI185172	BI185172 UNL-P-FN-	C 465	23.4	33.0	389	9	AA534063	AA534063 n97c04.s
C 393	23.6	33.2	683	12	AC132858	AC132858 Pan treq1	C 466	23.4	33.0	390	9	AI810599	AI810599 tu01g02.x
C 394	23.6	33.2	689	12	AQ482454	AQ482454 RPT-1172	C 467	23.4	33.0	390	10	C97720	C97720 C97720 Rice
C 395	23.6	33.2	705	10	BI654925	BI654925 603282879	C 468	23.4	33.0	393	9	AW800813	AW800813 MK3-OM006
C 396	23.6	33.2	726	12	AQ331313	AQ331313 nbX00049M	C 469	23.4	33.0	393	9	AA593138	AA593138 ng02f06.s
C 397	23.6	33.2	737	10	BF404641	BF404641 UI-R-CAI-	C 470	23.4	33.0	393	10	BE722750	BE722750 191111 MA
C 398	23.6	33.2	775	10	BI288815	BI288815 603074960	C 471	23.4	33.0	396	9	AI188192	AI188192 qd66e02.x
C 399	23.6	33.2	790	12	CNS01MEU	AI170355 Tetradon	C 472	23.4	33.0	396	9	AI866906	AI866906 u012g03.x
C 400	23.6	33.2	793	10	BI183374	BI183374 UNL-P-FN-	C 473	23.4	33.0	397	9	AA411471	AA411471 zv27d01.s
C 401	23.6	33.2	820	12	A2126265	A2126265 OSJNB007	C 474	23.4	33.0	397	9	AA599342	AA599342 q935f12.s
C 402	23.6	33.2	838	10	BF104750	BF104750 601822423	C 475	23.4	33.0	397	9	AA628085	AA628085 ns67d02.s
C 403	23.6	33.2	879	10	BI837697	BI837697 603086554	C 476	23.4	33.0	400	9	AI201551	AI201551 q974g12.x
C 404	23.6	33.2	896	10	BI183684	BI183684 UNL-P-FN-	C 477	23.4	33.0	405	9	AA401287	AA401287 z63g07.x
C 405	23.6	33.2	908	10	BI558770	BI558770 603241491	C 478	23.4	33.0	410	9	AI289756	AI289756 qv91f06.x
C 406	23.6	33.2	916	10	BI958077	BI958077 HVSME001	C 479	23.4	33.0	415	9	AA703567	AA703567 z14c11.s
C 407	23.6	33.2	927	9	AL527283	AL527283 AL527283	C 480	23.4	33.0	415	9	AI125356	AI125356 qd92n09.x
C 408	23.6	33.2	937	10	BI958226	BI958226 HVSME001	C 481	23.4	33.0	415	10	N21064	N21064 yx47g10.s1
C 409	23.6	33.2	942	10	BF539195	BF539195 602053059	C 482	23.4	33.0	421	10	BM027803	BM027803 020 Inter
C 410	23.6	33.2	1391	12	AC079973	AC079973 Pan treq1	C 483	23.4	33.0	425	10	BE938518	BE938518 RCO-TN007
C 411	23.6	33.2	1398	10	BC025584	BC025584 602274503	C 484	23.4	33.0	427	9	AI880411	AI880411 at55c09.x
C 412	23.6	33.2	1512	10	BI489196	BI489196 603021413	C 485	23.4	33.0	427	9	AA259219	AA259219 nc17f05.x
C 413	23.6	33.2	1568	12	AC076526	AC076526 Pan treq1	C 486	23.4	33.0	430	12	AA032275	AA032275 HS_2194_B
C 414	23.6	33.2	1620	10	BE903393	BE903393 601675925	C 487	23.4	33.0	436	9	AI280662	AI280662 qu04d08.x
C 415	23.6	33.2	1664	10	BE962090	BE962090 601655162	C 488	23.4	33.0	439	10	BE806295	BE806295 213463 MA
C 416	23.4	33.0	117	9	AW865189	AW865189 PM3-SN002	C 489	23.4	33.0	439	10	R50336	R50336 yj59a03.s1
C 417	23.4	33.0	126	9	AA458880	AA458880 zxx8b07.s	C 490	23.4	33.0	440	9	AI301508	AI301508 qn44g10.x
C 418	23.4	33.0	187	9	AA585828	AA585828 oV43b10.x	C 491	23.4	33.0	440	10	BE771975	BE771975 CM3-F7010
C 419	23.4	33.0	228	10	BF092131	BF092131 RCO-TN007	C 492	23.4	33.0	446	9	AI076047	AI076047 oV60c12.x
C 420	23.4	33.0	241	9	AW428130	AW428130 64991 MAR	C 493	23.4	33.0	448	10	BS926320	BS926320 HNC51-I-B
C 421	23.4	33.0	243	9	AA659908	AA659908 nv03d02.s	C 494	23.4	33.0	450	10	N80216	N80216 zd19e04.s1
C 422	23.4	33.0	259	9	AA365426	AA365426 EST76376	C 495	23.4	33.0	450	12	AQ592474	AQ592474 HS_5455_A
C 423	23.4	33.0	260	9	AA541749	AA541749 n187b11.s	C 496	23.4	33.0	452	9	AI832585	AI832585 at77d04.x
C 424	23.4	33.0	266	9	AA316985	AA316985 EST18930	C 497	23.4	33.0	454	9	AI086832	AI086832 o257h02.x
C 425	23.4	33.0	273	9	AI817603	AI817603 wK39d05.x	C 498	23.4	33.0	454	12	AQ937398	AQ937398 NB2-007R
C 426	23.4	33.0	276	9	AW797008	AW797008 QV1-OM003	C 499	23.4	33.0	455	9	AI304521	AI304521 q054h03.x
C 427	23.4	33.0	281	9	AI685742	AI685742 t437f02.x	C 500	23.4	33.0	455	9	AI797199	AI797199 w63b11.s
C 428	23.4	33.0	281	9	AW016211	AW016211 UI-H-BIOP	C 501	23.4	33.0	455	9	AA455032	AA455032 zx96g08.s
C 429	23.4	33.0	287	10	BF386067	BF386067 UI-R-CAO-	C 502	23.4	33.0	457	9	AI282395	AI282395 qu93e01.x
C 430	23.4	33.0	289	9	AA578385	AA578385 n131c08.s	C 503	23.4	33.0	460	9	AI087181	AI087181 g259h06.x
C 431	23.4	33.0	291	9	AA348877	AA348877 EST55455	C 504	23.4	33.0	460	9	AA401077	AA401077 zu51f02.s
C 432	23.4	33.0	292	9	AI811810	AI811810 tW32d08.x	C 505	23.4	33.0	463	9	AI266127	AI266127 qp64d07.x
C 433	23.4	33.0	294	9	AW068126	AW068126 cN23e01.x	C 506	23.4	33.0	464	10	R51320	R51320 y972f05.s1
C 434	23.4	33.0	295	9	AA781200	AA781200 a124g04.s	C 507	23.4	33.0	466	9	AI371879	AI371879 ta06b04.x
C 435	23.4	33.0	303	9	AA853433	AA853433 NHTBCae05	C 508	23.4	33.0	466	10	BF055306	BF055306 7178a02.x
C 436	23.4	33.0	303	9	AI826654	AI826654 wK35g08.s	C 509	23.4	33.0	467	9	AI200366	AI200366 qf98b07.x
C 437	23.4	33.0	306	9	AA670072	AA670072 q937h06.s	C 510	23.4	33.0	468	9	AI749608	AI749608 at25b09.x
C 438	23.4	33.0	306	9	AA877166	AA877166 o1v7g06.s	C 511	23.4	33.0	471	12	AQ201171	AQ201171 RPTc11-46
C 439	23.4	33.0	309	9	AI886703	AI886703 wn18f09.x	C 512	23.4	33.0	472	9	AI080529	AI080529 oz63e04.x
C 440	23.4	33.0	314	9	AA503968	AA503968 nH39a09.s	C 513	23.4	33.0	473	9	BB839928	BB839928 BB839928
C 441	23.4	33.0	317	9	AA662264	AA662264 nU93b07.s	C 514	23.4	33.0	474	10	N29929	N29929 yw53a08.s1
C 442	23.4	33.0	317	9	AA232779	AA232779 zt48g07.r	C 515	23.4	33.0	474	10	BE843841	BE843841 RCO-TN007
C 443	23.4	33.0	322	9	AA578194	AA578194 n129h02.s	C 516	23.4	33.0	481	9	AA534237	AA534237 n70e07.s
C 444	23.4	33.0	322	9	AA578224	AA578224 n122a01.s	C 517	23.4	33.0	485	9	AI189885	AI189885 qd29b10.x
C 445	23.4	33.0	327	10	BF092984	BF092984 MR4-TN011	C 518	23.4	33.0	489	9	AA447630	AA447630 zw97c06.s
C 446	23.4	33.0	328	9	AA285101	AA285101 zt23c03.r	C 519	23.4	33.0	490	9	AA834008	AA834008 of25a10.s
C 447	23.4	33.0	331	9	AI798639	AI798639 wG35g10.x	C 520	23.4	33.0	491	9	AI284586	AI284586 qu10c04.x
C 448	23.4	33.0	344	10	F21073	F21073 HSPD0541 H	C 521	23.4	33.0	492	9	AA552327	AA552327 nK06h12.s
C 449	23.4	33.0	348	9	AI273009	AI273009 qv63f07.x	C 522	23.4	33.0	497	9	AA600270	AA600270 af01e11.s
C 450	23.4	33.0	352	9	AA427777	AA427777 zw33g10.s	C 523	23.4	33.0	502	9	AA659536	AA659536 n03c01.s
C 451	23.4	33.0	352	9	AA515428	AA515428 nI69c08.s	C 524	23.4	33.0	505	9	AA695165	AA695165 ou54c12.s
C 452	23.4	33.0	360	9	AA533702	AA533702 nI92a11.s	C 525	23.4	33.0	506	9	AA743928	AA743928 ob05d12.s
C 453	23.4	33.0	363	9	AI239427	AI239427 qH31b05.x	C 526	23.4	33.0	508	9	AI749142	AI749142 at29g06.x
C 454	23.4	33.0	370	9	AI866979	AI866979 wn14d02.x	C 527	23.4	33.0	512	10	BS910359	BS910359 60280573
C 455	23.4	33.0	373	10	BF115460	BF115460 7n83c07.x	C 528	23.4	33.0	513	9	AW339871	AW339871 na61a01.x

529	23.4	33.0	514	9	A1288407	qV89b04.x	C 602	23.4	33.0	908	10	BF315427	BF315427	601899240
530	23.4	33.0	515	9	AA564063	nj03c02.s	C 603	23.4	33.0	924	10	BF966418	BF966418	602287016
531	23.4	33.0	515	10	BE501657	h162b01.x	C 604	23.4	33.0	1004	10	B1488417	B1488417	603020915
532	23.4	33.0	516	9	AA437391	zw25h08.s	C 605	23.4	33.0	1093	10	B1490590	B1490590	603032243
533	23.4	33.0	517	9	AA496371	zv37e09.s	C 606	23.4	33.0	1104	10	Bg117157	Bg117157	602346434
C 534	23.4	33.0	517	9	AA533527	nj96d08.s	C 607	23.4	33.0	1186	10	B117106	B117106	602868209
535	23.4	33.0	518	9	AA427585	zw30b01.s	C 608	23.4	33.0	1410	10	BG714387	BG714387	602669707
536	23.4	33.0	518	9	AA525853	n193b12.s	C 609	23.4	33.0	1788	10	BF572288	BF572288	602077734
537	23.4	33.0	518	10	W81224	zds5e08.s1	C 610	23.2	32.7	188	10	BE468846	BE468846	175166.BA
538	23.4	33.0	518	10	BE628128	HVSMED000	C 611	23.2	32.7	241	10	B1610768	B1610768	RH16534.S
539	23.4	33.0	521	9	A1521390	L105h04.x	C 612	23.2	32.7	246	10	BG690435	BG690435	338979.BA
540	23.4	33.0	523	9	A1367324	qv95a01.x	C 613	23.2	32.7	251	10	F10372	F10372	HSC3EB102.n
541	23.4	33.0	524	9	A1635503	ts65h12.x	C 614	23.2	32.7	262	9	BB595268	BB595268	BB595268
542	23.4	33.0	528	9	AA932637	coo5b04.s	C 615	23.2	32.7	267	10	B1976368	B1976368	485227.MA
543	23.4	33.0	529	9	AA954972	op24c10.s	C 616	23.2	32.7	296	9	A1200966	A1200966	qf68603.x
544	23.4	33.0	535	9	A1191324	qe48d05.x	C 617	23.2	32.7	296	9	BB108942	BB108942	BB108942
545	23.4	33.0	538	9	AL048329	DKEPSP56B	C 618	23.2	32.7	340	10	BF602245	BF602245	267430.MA
546	23.4	33.0	539	9	AA936956	oo65e10.s	C 619	23.2	32.7	351	10	BF602245	BF602245	267430.MA
C 547	23.4	33.0	540	9	A1222841	qp39g07.x	C 620	23.2	32.7	352	10	BF822879	BF822879	MRI-RT007
C 548	23.4	33.0	548	10	BE395678	601309670	C 621	23.2	32.7	352	10	BF823196	BF823196	MRI-RT007
C 549	23.4	33.0	550	10	BE391165	601286734	C 622	23.2	32.7	362	10	BF983191	BF983191	602308213
550	23.4	33.0	552	9	AA598926	ag24f04.s	C 623	23.2	32.7	377	9	AJ280791	AJ280791	4A3A-AAT-
551	23.4	33.0	554	9	A1459873	ar83c10.x	C 624	23.2	32.7	394	9	AA395502	AA395502	27285.Lam
552	23.4	33.0	555	9	A1707459	as90e07.x	C 625	23.2	32.7	397	10	BM375425	BM375425	EBEm06_SQ
553	23.4	33.0	557	9	A1672913	we74a08.x	C 626	23.2	32.7	401	9	AL449633	AL449633	AL449633
554	23.4	33.0	558	9	A1769112	wg32h06.x	C 627	23.2	32.7	445	10	BM368328	BM368328	EBed01.SQ
555	23.4	33.0	559	9	AM068546	cn21a11.x	C 628	23.2	32.7	464	10	BB796203	BB796203	BB796203
556	23.4	33.0	560	10	BM190310	POSM01000	C 629	23.2	32.7	464	10	H78033	H78033	yu85d12.r1
557	23.4	33.0	563	9	A1267900	qoz2h09.x	C 630	23.2	32.7	466	10	BG691772	BG691772	341098.BA
558	23.4	33.0	563	9	AA541667	n188f04.s	C 631	23.2	32.7	467	10	BM029732	BM029732	488070.MA
559	23.4	33.0	567	9	AM518701	xs89e12.x	C 632	23.2	32.7	474	9	AL500762	AL500762	AL500762
560	23.4	33.0	568	9	A1188975	qdz2c09.x	C 633	23.2	32.7	474	9	AL500428	AL500428	AL500428
561	23.4	33.0	568	9	AM008141	vw50e11.x	C 634	23.2	32.7	475	9	AL505305	AL505305	AL505305
562	23.4	33.0	569	9	AA541745	ni87b04.s	C 635	23.2	32.7	475	10	BE412626	BE412626	MCG001.G0
563	23.4	33.0	571	9	AA706831	zj30f06.s	C 636	23.2	32.7	477	9	AL502577	AL502577	AL502577
564	23.4	33.0	572	9	AA594873	no21e08.s	C 637	23.2	32.7	490	12	AQ149125	AQ149125	HS_3165_A
565	23.4	33.0	573	9	AA541782	n187g09.s	C 638	23.2	32.7	493	9	AV911975	AV911975	AV911975
566	23.4	33.0	574	9	AA595194	no32f08.s	C 639	23.2	32.7	494	9	AW369399	AW369399	OVI-BN000
C 567	23.4	33.0	578	10	BM073281	MEST63-FL	C 640	23.2	32.7	498	10	BM430021	BM430021	10no28EB
568	23.4	33.0	585	9	A1185277	qe31d10.s	C 641	23.2	32.7	500	12	AQ374839	AQ374839	RCCT11-14
569	23.4	33.0	590	9	AA595291	no35c01.s	C 642	23.2	32.7	510	10	BG246054	BG246054	602358887
570	23.4	33.0	595	9	A1749865	at33d12.x	C 643	23.2	32.7	513	12	AQ149120	AQ149120	HS_3165_A
571	23.4	33.0	596	9	AM514815	xu88f04.x	C 644	23.2	32.7	514	9	AV909875	AV909875	AV909875
572	23.4	33.0	601	9	AL515013	AL515013	C 645	23.2	32.7	515	12	AQ149124	AQ149124	HS_3165_A
573	23.4	33.0	602	9	A1457407	l173d07.x	C 646	23.2	32.7	518	12	AZ601326	AZ601326	1M0419K01
574	23.4	33.0	602	9	AA600983	nj28c03.s	C 647	23.2	32.7	533	9	BE129089	BE129089	894020B03
C 575	23.4	33.0	634	10	BM080795	MEST113-E	C 648	23.2	32.7	540	10	BM254132	BM254132	515480.MA
576	23.4	33.0	635	9	AA905294	o396c09.s	C 649	23.2	32.7	541	10	BM087329	BM087329	500073.MA
577	23.4	33.0	637	10	BF569958	602186119	C 650	23.2	32.7	550	12	AQ141621	AQ141621	HS_3164_A
578	23.4	33.0	641	9	A1299951	qns9d02.x	C 651	23.2	32.7	555	10	BE293593	BE293593	601186770
C 579	23.4	33.0	646	9	AM950053	EST362243	C 652	23.2	32.7	559	10	B1344776	B1344776	373343.MA
C 580	23.4	33.0	649	9	A1796694	wh59g03.x	C 653	23.2	32.7	576	9	AA149637	AA149637	z139B08.S
C 581	23.4	33.0	651	10	BG387129	602455844	C 654	23.2	32.7	580	9	AV919381	AV919381	AV919381
C 582	23.4	33.0	667	10	B1331818	602982391	C 655	23.2	32.7	584	10	BG699939	BG699939	602681114
C 583	23.4	33.0	683	9	AL636704	AL636704	C 656	23.2	32.7	592	10	B1569114	B1569114	RH01302.3
C 584	23.4	33.0	684	10	BF970507	602272686	C 657	23.2	32.7	594	9	AL500732	AL500732	AL500732
C 585	23.4	33.0	690	12	CNS01RL	AL164082	C 658	23.2	32.7	600	9	A1402072	A1402072	GHO7283.3
C 586	23.4	33.0	698	9	AV710372	AV710372	C 659	23.2	32.7	614	9	A1135299	A1135299	GH12978.5
C 587	23.4	33.0	711	10	B1332966	602980089	C 660	23.2	32.7	649	10	B1821128	B1821128	603035008
C 588	23.4	33.0	729	10	B1873647	963110C06	C 661	23.2	32.7	678	12	AG920634	AG920634	AV920634
C 589	23.4	33.0	773	9	A1121713	qb99a09.x	C 662	23.2	32.7	681	9	AG140897	AG140897	Par.trog1
C 590	23.4	33.0	782	12	CNS01EB9	AL140326	C 663	23.2	32.7	686	12	BB615574	BB615574	BB615574
C 591	23.4	33.0	798	9	A1207840	ao89h07.x	C 664	23.2	32.7	687	9	AL505164	AL505164	AL505164
C 592	23.4	33.0	798	9	A1833019	at74c09.x	C 665	23.2	32.7	699	9	AQ689431	AQ689431	NDXB0079J
C 593	23.4	33.0	810	10	B1905134	603168523	C 666	23.2	32.7	734	12	AL523843	AL523843	AL523843
C 594	23.4	33.0	844	10	BE970772	60180128	C 667	23.2	32.7	737	9	BE412633	BE412633	MCG001.F1
C 595	23.4	33.0	846	10	BF139734	601785386	C 668	23.2	32.7	739	12	AZ210947	AZ210947	SP_0154.B
C 596	23.4	33.0	851	9	AL570439	AL570439	C 669	23.2	32.7	774	12	AG095950	AG095950	Par.trog1
C 597	23.4	33.0	864	10	BF795336	602260425	C 670	23.2	32.7	795	12	B1088888	B1088888	602854234
C 598	23.4	33.0	871	10	B1763382	603052622	C 671	23.2	32.7	809	10	B1908486	B1908486	603069249
C 599	23.4	33.0	883	10	BG118128	602344895	C 672	23.2	32.7	816	10	B1754349	B1754349	603023191
C 600	23.4	33.0	887	10	BF689120	602185195	C 673	23.2	32.7	856	10	BG402360	BG402360	602465947
C 601	23.4	33.0	891	10	BE540883	601063002	C 674	23.2	32.7	870	10			

C 675	23.2	32.7	879	12	CNS03CGK	AL237773 Tetraodon	C 748	23	32.4	500	10	BE495279	BE495279 WHE1268_H
C 676	23.2	32.7	891	12	CNS032PC	AL225129 Tetraodon	C 749	23	32.4	502	10	BI899025	BI899025 480875 MA
C 677	23.2	32.7	934	12	AZ546916	ENTDPT17TR	C 750	23	32.4	505	10	AI871114	AI871114 w179c07.x
C 678	23.2	32.7	948	10	BE249922	600942970	C 751	23	32.4	505	10	BI360371	BI360371 387249 MA
C 679	23.2	32.7	950	10	BE900875	601673873	C 752	23	32.4	506	10	BF834074	BF834074 RC3-HT023
C 680	23.2	32.7	963	9	AL542562	AL542562	C 753	23	32.4	506	10	B016069	B016069 B016069
C 681	23.2	32.7	968	10	BE034355	BE034355 603302243	C 754	23	32.4	506	12	AQ412279	AQ412279 RPCT-11-1
C 682	23.2	32.7	979	9	AL523849	AL523849	C 755	23	32.4	507	10	AI741752	AI741752 w922e08.x
C 683	23.2	32.7	982	12	CNS03CPO	AL328101 Tetraodon	C 756	23	32.4	511	10	B015975	B015975 B015975
C 684	23.2	32.7	999	12	CNS030CF	AL562722 Tetraodon	C 757	23	32.4	515	9	AI967925	AI967925 w11a02.x
C 685	23.2	32.7	1004	12	BM423806	BM423806 AGENCOURT	C 758	23	32.4	516	9	AI638781	AI638781 t132c04.x
C 686	23.2	32.7	1017	12	CNS0330M9	AL561222 Tetraodon	C 759	23	32.4	516	10	BF002145	BF002145 7999h08.x
C 687	23.2	32.7	1039	10	BE700694	BE700694 602128682	C 760	23	32.4	520	9	AM205490	AM205490 UT-H-B1-
C 688	23.2	32.7	1043	12	CNS02AMN	AL185854 Tetraodon	C 761	23	32.4	526	10	BI963910	BI963910 1e6e04.x
C 689	23.2	32.7	1062	10	BE578023	602091864	C 762	23	32.4	527	10	BE501473	BE501473 hw32d12.x
C 690	23.2	32.7	1101	12	CNS00DEJ	AL609092 Drosophila	C 763	23	32.4	530	9	AM027982	AM027982 w25909.x
C 691	23.2	32.7	1312	10	BE728662	601563942	C 764	23	32.4	533	9	AL595594	AL595594 AL595594
C 692	23.2	32.7	1440	12	AC079960	AC079960 Pan. trogl	C 765	23	32.4	535	10	B026603	B026603 B026603
C 693	23.2	32.7	1538	10	BE183050	BE183050 601809622	C 766	23	32.4	539	10	BE077914	BE077914 228104 MA
C 694	23.2	32.7	1599	10	BE754873	BE754873 208534 MA	C 767	23	32.4	544	9	AI937105	AI937105 wp73b08.x
C 695	23.2	32.7	207	10	BE874394	BE874394 IL3-ET011	C 768	23	32.4	545	10	BI430728	BI430728 949060B11
C 696	23.2	32.7	231	9	BE604678	BE604678 BB604678	C 769	23	32.4	547	10	BC300674	BC300674 HVSMB001
C 697	23.2	32.7	234	10	HE1158	HE1158 yu37f05.s1	C 770	23	32.4	562	9	AI971310	AI971310 wr27g09.x
C 698	23.2	32.7	293	10	W01132	W01132 y825911.e1	C 771	23	32.4	573	9	AV601137	AV601137 AV601137
C 699	23.2	32.7	299	9	AV543790	AV543790 AV543790	C 772	23	32.4	574	10	B015084	B015084 B015084
C 700	23.2	32.7	299	9	BB347824	BB347824 BB347824	C 773	23	32.4	583	10	BI396375	BI396375 949054E12
C 701	23.2	32.7	303	9	AM820835	RC2-ST030	C 774	23	32.4	584	9	AA042224	AA042224 24545 CD4
C 702	23.2	32.7	306	9	BB275536	BB275536 BB275536	C 775	23	32.4	592	10	B014899	B014899 B014899
C 703	23.2	32.7	306	10	C74759	C74759 C74759 R1CE	C 776	23	32.4	593	10	B014899	B014899 B014899
C 704	23.2	32.7	326	10	C75396	C75396 C75396 Huma	C 777	23	32.4	594	10	B016953	B016953 B016953
C 705	23.2	32.7	330	9	AI910489	AI910489 w131f03.x	C 778	23	32.4	602	12	FR0004192	FR0004192 B014778
C 706	23.2	32.7	337	10	BF432584	BF432584 naby1f03.x	C 779	23	32.4	615	10	B014778	B014778 B014778
C 707	23.2	32.7	339	12	AA037591	AA037591 CIT-HSP-2	C 780	23	32.4	617	10	BE903142	BE903142 601673288
C 708	23.2	32.7	341	9	BB274952	BB274952 BB274952	C 781	23	32.4	622	10	BG134458	BG134458 pg11n.pk0
C 709	23.2	32.7	346	9	AL042304	AL042304 DREZP434M	C 782	23	32.4	625	12	AC034707	AC034707 Pan. trogl
C 710	23.2	32.7	348	12	AA0195361	AA0195361 RPT111-46	C 783	23	32.4	626	9	AM057581	AM057581 wy61a11.x
C 711	23.2	32.7	367	9	AI082395	AI082395 ov21c03.x	C 784	23	32.4	637	10	B028656	B028656 B028656
C 712	23.2	32.7	368	10	BF874726	BF874726 IL3-ET011	C 785	23	32.4	644	10	BM425699	BM425699 pg12c.pk0
C 713	23.2	32.7	374	9	AJ395453	AJ395453 AJ395453	C 786	23	32.4	651	12	AC049100	AC049100 Pan. trogl
C 714	23.2	32.7	390	9	AM198289	pol-D.pk0	C 787	23	32.4	655	10	BE310176	BE310176 601092815
C 715	23.2	32.7	419	9	AM135559	UT-H-B1-	C 788	23	32.4	656	10	B024608	B024608 B024608
C 716	23.2	32.7	429	9	AI768179	AI768179 w982a12.x	C 789	23	32.4	656	12	AC060182	AC060182 Pan. trogl
C 717	23.2	32.7	431	9	AI394569	AI394569 t908c04.x	C 790	23	32.4	662	12	A2986490	A2986490 2M0268B12
C 718	23.2	32.7	433	10	BF457143	BF457143 UI-M-B21-	C 791	23	32.4	663	10	B027422	B027422 B027422
C 719	23.2	32.7	436	12	AA0337660	AA0337660 NB6-249R	C 792	23	32.4	663	10	B027497	B027497 B027497
C 720	23.2	32.7	444	12	AA0339475	AA0339475 NR1-181R	C 793	23	32.4	665	10	B021044	B021044 B021044
C 721	23.2	32.7	446	12	AZ607189	AZ607189 LM0429E05	C 794	23	32.4	666	10	B017293	B017293 B017293
C 722	23.2	32.7	446	12	AA0192603	AA0192603 HS-2247-B	C 795	23	32.4	671	10	BI394478	BI394478 pg01n.pk0
C 723	23.2	32.7	449	9	AM55585	AM555858 p11c.pk0	C 796	23	32.4	674	10	B027719	B027719 B027719
C 724	23.2	32.7	450	9	AM270951	AM270951 x806f08.x	C 797	23	32.4	675	10	B014487	B014487 B014487
C 725	23.2	32.7	456	9	AI452771	AI452771 t145d01.x	C 798	23	32.4	675	10	B0207035	B0207035 B0207035
C 726	23.2	32.7	458	10	BE855473	BE855473 7914g01.x	C 799	23	32.4	682	10	BI256652	BI256652 602973951
C 727	23.2	32.7	459	9	AM193728	AM193728 xm29h04.x	C 800	23	32.4	683	10	B021484	B021484 B021484
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C 729	23.2	32.7	463	10	BE659920	BE659920 T9ESTZYAO	C 802	23	32.4	689	9	AL627746	AL627746 AU627746
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C 738	23.2	32.7	481	12	BE221731	BE221731 h558e10.x	C 811	23	32.4	774	10	BE525901	BE525901 602069682
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830	23	32.4	987	12	AG081063	AG081063	Par trogl	903	22.8	32.1	687	10	BJ005507
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867	22.8	32.1	447	9	AA111574	AA111574	MT4958.mo	940	22.8	32.1	957	10	BF308474
868	22.8	32.1	464	12	AZ489690	AZ489690	1M0322114	941	22.8	32.1	969	12	AG061086
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870	22.8	32.1	499	10	BM175069	BM175069	TGFEStyB1	943	22.8	32.1	981	10	BG247009
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## ALIGNMENTS

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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969	22.6	31.8	266	10	AA4473						
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ACCESSION B82759  
VERSION B82759.1  
KEYWORDS GI:2869782  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 520)  
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,F., Wible,C., de Jong,P. and Venter,J.C.  
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)  
JOURNAL Unpublished (1998)  
COMMENT Other GSSs: RPK11-17K22.TVB  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdamas@tigr.org  
Clones are derived from the human BAC library RPK1-11. For BAC library availability, please contact Pieter de Jong (pieter@edj.med.bufileo.edu). Clones may be purchased from BACAC Resources (http://bacpac.med.bufileo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/hungen/bac\_end\_search/bac\_end\_search.html  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
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/clone="11b"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; RPK11 Human Male BAC Library"  
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ORIGIN  
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Best local similarity 100.0%; Pred. No. 1.9e-10;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCAACCTGTCGACCGATCGTCGACCGACCGACCGCTGGCGGAGACAGCGCTGT 60  
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DB 355 GCACCTGTCGACCGATCGTCGACCGACCGACCGCTGGCGGAGACAGCGCTGT 296  
QY 61 GCCCTCCGAC 71  
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DB 295 GCCCTCCGAC 285  
RESULT 2  
LOCUS B858668  
DEFINITION B858668 RIKEN full-length enriched, adult male hypothalamus Mus  
ACCESSION B858668  
VERSION B858668.2  
KEYWORDS GI:16449788  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 657)  
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Koude,M., Koyama,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sasaki,O., Shikata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.  
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
JOURNAL Unpublished (2001)  
COMMENT On Nov 30, 2000 this sequence version replaced gi:11485212.  
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Email: genome-resgsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci,P., Shibata,Y., Hayashizaki,Y., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1611-1630 (2000)  
Wagl,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.







DEFINITION Fugu rubripes GSS sequence, clone 089D07b9, genomic survey sequence.  
ACCESSION AL126503  
VERSION AL126503.1 GI:6108118  
KEYWORDS GSS; genome survey sequence.  
SOURCE Takifugu rubripes.  
ORGANISM Takifugu rubripes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes; Tetraodontidae; Takifugu.  
REFERENCE 1 (bases 1 to 605)  
AUTHORS Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K., Umanian,Y., Williams,G. and Brenner,S.  
TITLE Direct Submission  
JOURNAL Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK Email: biohelp@hmp.mrc.ac.uk  
Vektor: pBluescript II KS  
V type: phagemid  
PRIMER: KS  
COMMENT DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.  
FEATURES  
Source 1..605  
/organism="Takifugu rubripes"  
/db\_xref="taxon:3103"  
/clone\_lib="cosmid 089D07"  
/clone="089D07b9"  
BASE COUNT 123 a 189 c 180 g 92 t 21 others  
ORIGIN  
Query Match 38.9%; Score 27.6; DB 12; Length 605;  
Best Local Similarity 72.0%; Pred. No. 3.1e+02;  
Matches 36; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
Oy 4 ACCTGCGAGCCGATGCGCGACCGACCGACTGGGCGGAGAGAC 53  
|||||  
Db 89 ACCGAGCTGACCCGTCGCGACCGACCGACCGCTCTGGACCGAGCGAC 138  
|||||  
RESULT 8  
LOCUS BF305771 921 bp mRNA linear EST 21-NOV-2000  
DEFINITION 601889127P1 NIH\_MGC\_17 Homo sapiens cDNA clone IMAGE:4122991 5', mRNA sequence.  
ACCESSION BF305771  
VERSION BF305771.1 GI:11252767  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 921)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs@email.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Prepared by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov  
Plate: LNCMI007 row: e column: 08  
High quality sequence stop: 692.  
FEATURES  
Source 1..921  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4122991"  
DEFINITION Fugu rubripes GSS sequence, clone 089D07b9, genomic survey sequence.  
ACCESSION AL126503  
VERSION AL126503.1 GI:6108118  
KEYWORDS GSS; genome survey sequence.  
SOURCE Takifugu rubripes.  
ORGANISM Takifugu rubripes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes; Tetraodontidae; Takifugu.  
REFERENCE 1 (bases 1 to 605)  
AUTHORS Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K., Umanian,Y., Williams,G. and Brenner,S.  
TITLE Direct Submission  
JOURNAL Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK Email: biohelp@hmp.mrc.ac.uk  
Vektor: pBluescript II KS  
V type: phagemid  
PRIMER: KS  
COMMENT DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.  
FEATURES  
Source 1..605  
/organism="Takifugu rubripes"  
/db\_xref="taxon:3103"  
/clone\_lib="cosmid 089D07"  
/clone="089D07b9"  
BASE COUNT 123 a 189 c 180 g 92 t 21 others  
ORIGIN  
Query Match 38.9%; Score 27.6; DB 12; Length 605;  
Best Local Similarity 72.0%; Pred. No. 3.1e+02;  
Matches 36; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
Oy 4 ACCTGCGAGCCGATGCGCGACCGACCGACTGGGCGGAGAGAC 53  
|||||  
Db 89 ACCGAGCTGACCCGTCGCGACCGACCGACCGCTCTGGACCGAGCGAC 138  
|||||  
RESULT 9  
LOCUS B615009 848 bp mRNA linear EST 18-APR-2001  
DEFINITION 602644283P1 NIH\_MGC\_61 Homo sapiens cDNA clone IMAGE:4775061 5', mRNA sequence.  
ACCESSION B615009  
VERSION B615009.1 GI:13666380  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 848)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs@email.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov  
Plate: LNCMI649 row: f column: 22  
High quality sequence stop: 550.  
FEATURES  
Source 1..848  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4775061"  
/clone\_lib="NIH\_MGC\_61"  
/tissue\_type="embryonal carcinoma"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggcggcggcggc); Site\_2: SfiI (ggcattatggc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCGCATTAATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGCGGCGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC

BASE COUNT 214 a 234 c 242 g 158 t  
ORIGIN

Query Match 38.0%; Score 27; DB 10; Length 848;  
Best Local Similarity 62.7%; Pred. No. 4.8e+02;  
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 2 CAACGTCTCCGACCATGCGTCCGACCAACCGACCGCTGGCGGAGAGACAGCCTGTG 61  
Db 655 CCACGGGGCGCCGACACAGCGGGCCCGGACTGCGAGGACCTATGACGAAACTGCGAGAG 714

QY 62 CCCTCCG 68  
Db 715 CCTACCG 721

RESULT 10  
BF527152 673 bp mRNA linear EST 11-DEC-2000  
LOCUS 602039822F2 NCI\_CGAP\_Brn67 Homo sapiens CDNA clone IMAGE:4177685  
DEFINITION 5', mRNA sequence.  
ACCESSION BF527152  
VERSION BF527152.1 GI:11614515  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 673)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@rs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM9484 row: 1 column: 06  
High quality sequence stop: 143.  
Location/Qualifiers  
1. 673  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1ib="NCI\_CGAP\_Brn67"  
/issue\_type="anaplastic oligodendroglioma with 1p/19q  
loss"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: brain; Vector: pCMV-SPOK6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: oligo dt.  
Average insert size 2.3 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 105 a 167 c 273 g 128 t  
ORIGIN

Query Match 37.5%; Score 26.6; DB 10; Length 673;  
Best Local Similarity 66.7%; Pred. No. 6e+02;  
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 TGTCCGACCATGCGTCCGACCGACCGACTGGCGGAGAGACAGCCTGTGCC 63  
Db 48 TCTCCACCCAGCGCTCTGTGCGGTGACGCTGAGCGGAGACCGGCTGTGGC 104

RESULT 11  
BF541519 799 bp mRNA linear EST 11-DEC-2000  
LOCUS 602067882F1 NIH\_MGC\_58 Homo sapiens CDNA clone IMAGE:4066892 5',  
DEFINITION

ACCESSION mRNA sequence.  
BF541519  
VERSION BF541519.1 GI:11628900  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 799)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@rs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM905 row: c column: 21  
High quality sequence stop: 524.  
Location/Qualifiers  
1. 799  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1ib="IMAGE:4066892"  
/clone\_1ib="NIH\_MGC\_58"  
/issue\_type="hypernephroma"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: kidney; Vector: pNR-LIB (Clontech); Site\_1:  
SfiI (ggccgctcgcc); Site\_2: SfiI (ggccatctagcc);  
Double-stranded CDNA was prepared from cell line RNA. 5'  
and 3' adaptors were used in cloning as follows: 5'  
sequence: 5'-ATTCTAGAGCGCCGAGCGCCGACATG-dT(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."

BASE COUNT 270 a 161 c 161 g 207 t  
ORIGIN

Query Match 37.5%; Score 26.6; DB 10; Length 799;  
Best Local Similarity 63.1%; Pred. No. 6.1e+02;  
Matches 41; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 4 ACCTGTCCGACCATGCGTCCGACCGACCGACTGGCGGAGAGACAGCCTGTGCC 63  
Db 773 ACCGGCCGACCATGCGTCCGACCGCGCCGCTTTTGGGAGACCGCCTGTGCT 714

QY 64 CTCCG 68  
Db 713 GCCCG 709

RESULT 12  
BF382133 894 bp mRNA linear EST 27-NOV-2000  
LOCUS 601814891F2 NIH\_MGC\_56 Homo sapiens CDNA clone IMAGE:4048894 5',  
DEFINITION mRNA sequence.  
ACCESSION BF382133  
VERSION BF382133.1 GI:11363436  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 894)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LICM880 row: e column: 23  
High quality sequence stop: 425.

FEATURES  
source

Location/Qualifiers  
1..894  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:404894"  
/clone\_lib="NIH\_MGC\_56"  
/lssuse\_type="Primitive neuroectoderm"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (99cgcgcgcgc); Site\_2: SfiI (99ccatcgcgc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT  
ORIGIN  
249 a 234 c 238 g 173 t

Query Match 37.5%; Score 26.6; DB 10; Length 894;  
Best Local Similarity 63.1%; Pred. No. 6.2e+02;  
Matches 41; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 2 CAACGTGCGACCCATCGCTCCGACCGACGACCTGGCGGAGACAGACGCTGTG 61

Db 206 CAGGCTGCGACCATTCCTCGCTCAGCTCCGAGTACCTGGACCTGTCACTG 147

QY 62 CCCTC 66

Db 146 CCCCC 142

RESULT 13  
CNS02R80/c  
LOCUS  
DEFINITION  
CNS02R80 909 bp DNA linear GSS 14-MAY-2000  
Tetraodon nigroviridis genome survey sequence PUC-ori end of clone  
159B11 of library G from Tetraodon nigroviridis, genomic survey  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AL210273  
GI:7869092  
GSS: genome survey sequence.  
Tetraodon nigroviridis.  
Tetraodon nigroviridis.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.

REFERENCE  
AUTHORS  
1 (bases 1 to 909)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
2 (bases 1 to 909)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Bonneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Mincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.

TITLE

Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
3 (bases 1 to 909)  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.

FEATURES  
source

Location/Qualifiers  
1..909  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="159B11"  
/clone\_lib="G"  
/note="Genoscope sequence ID : COAG159CA06SP1-end ;  
PUC-ori"

BASE COUNT  
ORIGIN  
170 a 256 c 287 g 171 t 25 others

Query Match 37.5%; Score 26.6; DB 12; Length 909;  
Best Local Similarity 60.9%; Pred. No. 6.2e+02;  
Matches 42; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

QY 3 AACCTGTCGACCCATCGCTCCGACCGACGACCTGGCGGAGACAGACGCTGTG 62

Db 380 AACGCTTCGACCCAGACGCGGCTCCGCGACCTGGACGAGAGACAGCCCTCG 321

QY 63 CCTCGACC 71

Db 320 CCGCGGVC 312

RESULT 14  
BG697293/c  
LOCUS  
DEFINITION  
BG697293 937 bp mRNA linear EST 07-MAY-2001  
602660543P1 NCL\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4803466 5',  
mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
BG697293  
GI:13963352  
EST.  
human.  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 937)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LRAM10699 row: f column: 11  
High quality sequence stop: 857.

FEATURES  
source  
Location/Qualifiers  
1..937  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4803466"  
/clone\_lib="NCI CGAP\_Skn3"  
/lab\_host="DH10B (TI phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT	165 a	276 c	326 g	170 t
ORIGIN				
Query Match				
Best Local Similarity	37.5%	Score 26.6:	DB 10:	Length 937:
Matches	41:	Conservative 0:	Mismatches 24:	Indels 0:
DB	115	ACCGTGTCCCGCCACCGGGTCTTACACAGGGGACCTGACTGTGTCTCAACCTGTCC	56	
QY	63	CCTCC 67		
Db	55	CCGCC 51		
RESULT 15				
LOCUS	BF583863	416 bp	mRNA	linear
DEFINITION	602096861F1 NCI_CGAP_CO24 Mus musculus CDNA clone IMAGE:4216815 5'			
ACCESSION	BF583863			
VERSION	BF583863.1	GI:11657581		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 416)			
TITLE	NIH-MGC http://mgc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM9794 row: j column: 16 High quality sequence stop: 336. Location/Qualifiers 1. 416 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:4216815" /clone_lib="NCI_CGAP_CO24" /lab_host="DH10B (TI phage-resistant)" /note="Organ: colon; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library." BASE COUNT 65 a 147 c 112 g 92 t ORIGIN			
Query Match				
Best Local Similarity	36.9%	Score 26.2:	DB 10:	Length 416:
Matches	40:	Conservative 0:	Mismatches 23:	Indels 0:
QY	61	GCC 63		
Db	110	CCC 112		
RESULT 16				
LOCUS	AL515844/c			

LOCUS	AJ551844	811 bp	mRNA	linear	EST 16-FEB-2001
DEFINITION	AJ551844 LTR1.NFL006.PL2 Homo sapiens cDNA clone CS0D1061YD17 5 prime, mRNA sequence.				
ACCESSION	AJ551844				
VERSION	AJ551844.1	GI:12890181			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 811)				
AUTHORS	Li,W.B., Gruber,C., Jesssee,J. and Polayes,D.				
TITLE	Full-length cDNA libraries and normalization unpublished (2001)				
JOURNAL					
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers				
FEATURES	1..811				
SOURCE	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS0D1061YD17" /clone_id="LTR1.NFL006.PL2" /tissue_type="Placenta" /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NOTI-01io(dT) primer. Five prime end enriched, double-stranded and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. Contact : Peng Liang Life Technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"				
BASE COUNT	125 a	215 c	249 g	167 t	55 others
ORIGIN					
	Query Match. 36.9%; Score 26.2; DB 9; Length 811; Best Local Similarity 58.0%; Pred. NO. 8e+02;				
	Matches 40; Conservative 3; Mismatches 26; Indels 0; Gaps 0;				
DQ	3 AACGCTCCGACCATTGGGTCCGAACCGCACCCAGCTGGCGGAGAGACAGCCTGRGC	62			
DB	462 MACCTGYTAGCCCTTCCTCCCTCGGCCAGACCTCAGAGCCAGCAGGACCCCTCTGTTGG	403			
QY	63 CCTCGACC	71			
DB	402 CCTCGRC	394			
RESULT 17					
LOCUS	AM427436/c	200 bp	mRNA	linear	EST 25-APR-2001
DEFINITION	61386 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.				
ACCESSION	AM427436				
VERSION	AM427436.1	GI:6955383			
KEYWORDS	EST.				
SOURCE	cow.				
ORGANISM	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 200)				
AUTHORS	Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.R., Rohrer,G.A., Chitko-Mckown,C.G.,... Pette,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.				
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle				
JOURNAL	Genome Res. 11 (4), 626-630 (2001)				
MEDLINE	21180013				

COMMENT Contact: Smith TPL  
USA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smithemail@marc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 20  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCAGTCAGCAG  
Plate: 32 row: F column: 23  
Seq primer: ATTAGTGACACTATAG.  
FEATURES  
Location/Qualifiers  
1..200  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="MARC 3BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinosus muscle, and fetal  
longissimus muscle."  
BASE COUNT 46 a 53 c 52 g 49 t  
ORIGIN  
Query Match 36.6%; Score 26; DB 9; Length 200;  
Best Local Similarity 65.5%; Pred. No. 7.7e+02;  
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
OY 5 CCTGCGCAGCCGCTCGCGACCGACCGACCTGGCGCGGAGACAGCGCTGTGC 62  
|||||  
Db 58 CCGTGCGTCCGCTCGCTCGCCAGTGGCGAGCACTGGAGGAGACAGCGCTGTGC 1  
|||||  
RESULT 18 323 bp DNA linear GSS 17-DEC-2001  
A2919994/c LOCUS 1006017F03.y1 1006 - Rescuemu Grid G Zea mays genomic, DNA  
DEFINITION sequence.  
ACCESSION A2919994  
VERSION A2919994.1 GI:13390260  
KEYWORDS GSS.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 323)  
REFERENCE 1  
AUTHORS Walbot,V.  
TITLE Maize genomic sequences found using engineered Rescuemu transposon  
JOURNAL Unpublished (2001)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Very probable ligation site of ends cut by a single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1006017 row: 37  
Class: transposon-tagged.  
FEATURES  
Location/Qualifiers  
1..323  
/organism="Zea mays"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/clone\_lib="1006 - Rescuemu Grid G"  
/tissue\_type="leaf"  
/dev\_stage="adult"

/lab\_host="DH10B"  
/note="Organ: leaf; Vector: Rescuemu (engineered from  
pBluescript backbone); Site\_1: BamHI; Site\_2: BglII;  
Rescuemu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on Rescuemu, go to the web  
site 'www.zmdb.iastate.edu' and follow the links for  
'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was  
extracted from leaf punches, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."  
BASE COUNT 39 a 78 c 125 g 81 t  
ORIGIN  
Query Match 36.6%; Score 26; DB 12; Length 323;  
Best Local Similarity 65.5%; Pred. No. 8.1e+02;  
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
OY 8 GTCCGACCATCGCTCCGACCGACCGACCTGGCGCGGAGACAGACCTGTGCTT 65  
|||||  
Db 123 GTCTTCTCGCTCGCTCCGACCGACCGACCGAGCGCGCGCTTCACT 66  
|||||  
RESULT 19 751 bp mRNA linear EST 15-MAY-2001  
BG756483 LOCUS 602715622F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4855829 5',  
DEFINITION mRNA sequence.  
ACCESSION BG756483  
VERSION BG756483.1 GI:14067136  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 751)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMU at:  
http://image.llnl.gov  
Plate: L10M1705 row: 1 column: 06  
High quality sequence stop: 734.  
FEATURES  
Location/Qualifiers  
1..751  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:4855829"  
/clone\_lib="NIH\_MGC\_48"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."  
BASE COUNT 182 a 202 c 216 g 151 t  
ORIGIN  
Query Match 36.6%; Score 26; DB 10; Length 751;

Best Local Similarity 62.1%; Pred. No. 9e+02;  
Matches 41; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 6 CTTCCGACCGATCGGTCCGACCGACCGACCGGCGGAGAGACACCTGTGCTT 65  
Db 78 CTACCGACCGACCGACCGCGCGCGTGTCCCGGTGCGAGCGCCCGCGCGCC 137

QY 66 CCGACC 71  
Db 138 CCGATC 143

RESULT 20  
BF167284 779 bp mRNA linear EST 30-OCT-2000  
LOCUS 601775758F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:4017351 5',  
DEFINITION mRNA sequence.  
ACCESSION BF167284  
VERSION BF167284.1 GI:11047636  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgabs@emil.nih.gov](mailto:cgabs@emil.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LLM9266 row: c column: 16  
High quality sequence start: 7  
High quality sequence stop: 627.  
Location/Qualifiers  
1..779  
/organism="Mus musculus"  
/strain="C57BL/6J (f1er1)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4017351"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary.  
Stem cell origin."  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: SalI;  
Site: 2: NotI. Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

BASE COUNT 197 a 225 c 220 g 137 t

ORIGIN  
Query Match 36.6%; Score 26; DB 10; Length 779;  
Best Local Similarity 65.5%; Pred. No. 9e+02;  
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 12 GACCCATCGGTCCGACCGACCGACCGGCGGAGAGACCGCTGTGCTTCCGA 69  
Db 93 GAACCCAGAGCGCGGACCTAGACCGACCGTGGAGCGACTACAGCGCTGTGCGACCA 150

RESULT 21  
N30773 555 bp mRNA linear EST 05-JAN-1996  
LOCUS YW74907.s1 Soares,placenta,8to9weeks,2Nbp8to9w Homo sapiens cDNA  
DEFINITION clone IMAGE:258012.3' similar to gb: X07868.mal PUTATIVE  
INSULIN-LIKE GROWTH FACTOR II ASSOCIATED (HUMAN);, mRNA sequence.  
ACCESSION N30773

VERSION N30773.1 GI:1149293  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
1 (bases 1 to 555)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Matis, M., Parsons, J.,  
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston  
R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Willson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@wustl.edu](mailto:est@wustl.edu)  
High quality sequence stops: 388  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: m13 -40 forward  
High quality sequence stop: 388.  
Location/Qualifiers  
1..555  
/organism="Homo sapiens"  
/db\_xref="GDB:387622"  
/db\_xref="taxon:9606"  
/clone="IMAGE:258012"  
/clone\_lib="Soares,placenta,8to9weeks,2Nbp8to9w"  
/dev\_stage="two placentae: one from 8 weeks and another  
from 9 weeks post conception"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: placenta; Vector: pRTT3D (Pharmacia) with a  
modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st  
strand cDNA was primed with a Not I - Oligo(dT) primer [5'  
TCTTACCATCTGAGTGGAGCGGCGGAGATTTTCTTTTCTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pRTT3 vector  
(Pharmacia). Library constructed by Bento Soares and  
M.Felima Bonaldo."

BASE COUNT 100 a 154 c 177 g 121 t 3 others

ORIGIN  
Query Match 36.3%; Score 25.8; DB 10; Length 555;  
Best Local Similarity 60.9%; Pred. No. 9.9e+02;  
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 3 AACCTGTCGACCGATCGGTCCGACCGACCGACCGGCGGAGAGACACCTGTGCTG 62  
Db 432 AACCTGTCGACCGCTTCCCTCGCGACCGTACGCGACCGACCGCGCTGTGCTG 373

QY 63 CTTCCGACC 71  
Db 372 CTTCCGACC 364

RESULT 22  
AJ395984 631 bp mRNA linear EST 25-JAN-2001  
LOCUS AJ395984 dKfz426 Gallus gallus cDNA clone 24n20f1, mRNA sequence.  
ACCESSION AJ395984  
VERSION AJ395984.1 GI:7127460  
KEYWORDS EST.  
SOURCE chicken.  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 631)



	/lab_host="E. coli EMDH10B"
	/note="vector: PCMVSPORT6; Library made from equivalent
	pools of total RNA isolated from each tissue at different
	ages. Single pass sequencing from 5'-end"
BASE COUNT	106 a            229 c            196 g            116 t
ORIGIN	
Query Match	36.3%; Score 25.8; DB 10; Length 647;
Best Local Similarity	63.9%; Pred. No. 1e+03;
Matches 39; Conservative	0; Mismatches 22; Indels 0; Gaps 0;
OY	1 GCACCTGTCGCAGCCATCGGTCCGAACCGCAGCACTGGCGGAGAGACACTGT 60   Db 215 GCCACATACCACCACTGGCGGGGCTGTGACCTTCCACGCCCGGCGAGAGCACGCTTCT 274
OY	61 G 61
D	275 G 275
RESULT 24	
LOCUS	BF527152 673 bp mRNA linear EST 11-DEC-2000
DEFINITION	60203982F2 NCI_CGAP_Brn67 Homo sapiens cdNA clone IMAGE:4177685
VERSION	BF527152
KEYWORDS	5' mRNA sequence.
SOURCE	BF527152.1 GI:11614515
ORGANISM	EST. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 673) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: David N. Louis, M.D. CDNA Library Preparation: Life Technologies, Inc. DNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.nl.gov plate: LLM9484 row: 1 column: 06 High quality sequence stop: 143.
JOURNAL COMMENT	Location/Qualifiers 1..673 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4177685" /clone_lib="NCI CGAP_Brn67" /tissue_type="aneoplastic oligodendroglioma with lp/19q loss" /_lab_host="DH10B (T1 phage-resistant)" /_note="Organ: brain; Vector: pCMV-SPORT6; site_1: NotI; site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP Library."
BASE COUNT	105 a            167 c            273 g            128 t
ORIGIN	
Query Match	36.3%; Score 25.8; DB 10; Length 673;
Best Local Similarity	63.9%; Pred. No. 1e+03;
Matches 39; Conservative	0; Mismatches 22; Indels 0; Gaps 0;
OY	1 GCACCTGTCGCAGCCATCGGTCCGAACCGCAGCACTGGCGGAGAGACACTGT 60   Db 115 GCACAGCATCGCGACACCGGTCCCTCCCGTGACGCTGCACGCGACAGAGACCTTG 56
OY	61 G 61

Db	55	G	55
RESULT 25	AI373475	136 bp	mRNA
LOCUS	g246b05.x1	NCI-CGAP_Kid11	Homo sapiens cDNA clone IMAGE:2029905 3'
DEFINITION	mRNA sequence.		
ACCESSION	AI373475		
VERSION	AI373475.1	GI:4153341	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 136)		
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps@email.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://www-bio.llnl.gov/bbrp/image/image.html">www-bio.llnl.gov/bbrp/image/image.html</a> Seq primer: -40UP from GIBCO.		
FEATURES	Location/Qualifiers		
SOURCE	1..136		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2029905"		
	/clone_id="NCI CGAP_Kid11"		
	/lab_host="DH10B"		
	/note="Organ: kidney; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	24 a	42 c	41 g
ORIGIN			29 t
Query Match	36.1%;	Score 25.6;	DB 9;
Best Local Similarity	66.1%;	Pred. No. 9.5e+02;	
Matches 37;	Conservative 0;	Mismatches 19;	Indels 0;
			Gaps 0;
OY	1	GCACCTGTCGACCCATGCGTCCGACACCGCAGCAGCTGGCGGGAGACAGAC	56
Db	48	GCACACTGCTCCCTCCACAGGTGGGTGAGCCACGACGAGGAGGAGAGATCC	103
RESULT 26			
LOCUS	BF476113	136 bp	mRNA
DEFINITION	h277f04.x1	NCI-CGAP_Kid11	Homo sapiens cDNA clone IMAGE:3134527 3'
ACCESSION	BF476113		
VERSION	BF476113.1	GI:11546940	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota: Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 136)		
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps@email.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://www-bio.llnl.gov/bbrp/image/image.html">www-bio.llnl.gov/bbrp/image/image.html</a> Seq primer: -40UP from GIBCO.		
FEATURES	Location/Qualifiers		
SOURCE	1..136		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2029905"		
	/clone_id="NCI CGAP_Kid11"		
	/lab_host="DH10B"		
	/note="Organ: kidney; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	24 a	42 c	41 g
ORIGIN			29 t

AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CGNA Library Preparation: M. Bento Soares, Ph.D. CGNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLW, send email to: info@image.lnl.gov Seq primer: -40UP from Glbco. Location/Qualifiers 1. 136 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3134527" /clone_1ib="NCI_CGAP_K1411" /lab_host="DIH10B" /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_K143 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonesids 132376-1323911, 145607-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT	24 a 42 c 41 g 29 t
ORIGIN	
Query Match	36.1%; Score 25.6; DB 10; Length 136;
Best Local Similarity	66.1%; Pred. No. 9.5e+02;
Matches	37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
1	GCACCTGTCGACCCATGCGTCCGAAACCGACGACCTGCGGAGAGACAGC 56
111 111 11 111 11 111 11 111 111 11 111 11	
48	GCACACTGCCCTCCAGTGCGGTGAGAGCCAGCAGCAGGAGGAGAGAGATGC 103
RESULT 27	
LOCUS	AW513012 142 bp mRNA linear EST 03-MAR-2000
DEFINITION	AW513012.1 GI:7151090
ACCESSION	AW513012
VERSION	AW513012.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 142)
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CGNA Library Preparation: Life Technologies, Inc. CGNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLW, at: <a href="http://image.lnl.gov/image/html/resources.shtml">image.lnl.gov/image/html/resources.shtml</a> Seq primer: -40UP from Glbco. Location/Qualifiers
FEATURES	
source	

source 1. 142  
/organism="Homo sapiens"  
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/clone="IMAGE:2792386"  
/clone\_lib="NCI\_CGAP\_Ut1"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPOK6; Site:1: Salt;  
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

BASE COUNT 26 a 42 c 42 g 32 t

ORIGIN

Query Match 36.1%; Score 25.6; DB 9; Length 142;  
Best Local Similarity 66.1%; Pred. No. 9.6e+02;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 GCACCTGTCCGACCATGGCTCCGACCGCAGCAGTGGCGGAGACAGC 56  
111 111 11 1111 11 111 111111 111 1111 11

Db 51 GCACACTGCCCTTCCAGGTGGGTGAAGCCCGACGAGGAGGAGATGC 106

RESULT 28  
AM169520 144 bp mRNA linear EST 12-NOV-1999  
LOCUS xj29e01.x1 NCI\_CGAP\_Ut2 Homo sapiens cDNA clone IMAGE:2658648 3,  
DEFINITION mRNA sequence.  
ACCESSION AM169520  
VERSION AM169520.1 GI:6401128  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 144)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html

FEATURES  
source  
Possible reversed clone: polyT not found  
Seq primer: -40UP from Gibco.  
Location/Qualifiers  
1. 144  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2658648"  
/clone\_lib="NCI\_CGAP\_Ut2"  
/tissue\_type="moderately-differentiated endometrial  
adenocarcinoma, 3 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPOK6; Site:1: Salt;  
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

BASE COUNT 27 a 42 c 41 g 34 t

ORIGIN

Query Match 36.1%; Score 25.6; DB 9; Length 144;  
Best Local Similarity 66.1%; Pred. No. 9.6e+02;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 GCACCTGTCCGACCATGGCTCCGACCGCAGCAGTGGCGGAGACAGC 56  
111 111 11 1111 11 111 111111 111 1111 11

Db 53 GCACACTGCCCTTCCAGGTGGGTGAAGCCCGACGAGGAGGAGATGC 108

RESULT 29  
A1183699 258 bp mRNA linear EST 29-OCT-1998  
LOCUS gel5c07.x1 Soares\_fetal\_lung\_NBH119W Homo sapiens cDNA clone  
DEFINITION IMAGE:1739052 3', mRNA sequence.  
ACCESSION A1183699  
VERSION A1183699.1 GI:3734337  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 258)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 684 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 225.  
Location/Qualifiers  
1. 258  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1739052"  
/clone\_lib="Soares\_fetal\_lung\_NBH119W"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: p773D (Pharmacia) with a  
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer  
[5'-TGTTCCAACTCGAAGTGGAGCGGCCCAATTTTCTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified p773 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M. Fatima Bonaldo. This library was constructed  
from the same fetus as the fetal heart library, Soares  
fetal heart NBH119W."

BASE COUNT 49 a 79 c 82 g 48 t

ORIGIN

Query Match 36.1%; Score 25.6; DB 9; Length 258;  
Best Local Similarity 66.1%; Pred. No. 1e+03;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 GCACCTGTCCGACCATGGCTCCGACCGCAGCAGTGGCGGAGACAGC 56  
111 111 11 1111 11 111 111111 111 1111 11

Db 58 GCACACTGCCCTTCCAGGTGGGTGAAGCCCGACGAGGAGGAGATGC 113

RESULT 30  
A1183281 275 bp mRNA linear EST 18-MAR-1999  
LOCUS tc77d04.x1 Soares\_NhMPu\_S1 Homo sapiens cDNA clone IMAGE:2070631  
DEFINITION 3', mRNA sequence.  
ACCESSION A1183281  
VERSION A1183281.1 GI:4196062  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 275)  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
Insert Length: 392 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 274.  
Location/Qualifiers  
1. 275  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2070631"  
/clone\_lib="Soares-NHMP\_LSI"  
/tissue\_type="Pooled human melanocyte, fetal heart, and  
pregnant uterus"  
/lab\_host="DH10B"  
/note="Organ: mixed (see below); Vector: pT7T3D-Pac  
(Pharmacia) with a modified polylinker; Site\_1: Not I;  
Site\_2: Eco RI; Equal amounts of plasmid DNA from three  
normalized libraries (melanocyte 2NbHW, pregnant uterus  
NbHPV, and fetal heart NbH19M) were mixed, and ss circles  
were made in vitro. Following HAP purification, this DNA  
was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of I.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."  
BASE COUNT 58 a 84 c 94 g 39 t  
ORIGIN

Query Match 36.1%; Score 25.6; DB 9; Length 275;  
Best Local Similarity 66.1%; Pred. No. 1e+03;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 1 GCACCTGTCGACCCATCGGTCGACCGACCGACCTGGCGGAGACAGC 56  
39 GCACACTGCCCTTCCAGGTGGGTGAAGCCGACCGACGAGGAGGATGC 94

RESULT 31  
LOCUS AT1270131 282 bp mRNA linear EST 02-DEC-1998  
DEFINITION q163g06.x1 NCI-CGAP\_Eso2 Homo sapiens cDNA clone IMAGE:195994 3',  
mRNA sequence.  
ACCESSION AT1270131  
VERSION AT1270131.1 GI:3889298  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 282)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip  
Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.lnl.gov/bdrrp/image/image.html](http://www.bio.lnl.gov/bdrrp/image/image.html)  
Insert Length: 1470 Std Error: 0.00

Seq primer: -40UP from Gibco  
High quality sequence stop: 227.  
Location/Qualifiers  
1. 282  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:195994"  
/clone\_lib="NCI-CGAP\_Eso2"  
/tissue\_type="squamous cell carcinoma"  
/lab\_host="DH10B"  
/note="Organ: esophagus; Vector: PCMV-SPORT6; Site\_1: SalI  
; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo  
dT. Average Insert size 1.1 kb. Life Technologies catalog  
#: 11502-010"  
BASE COUNT 59 a 86 c 93 g 44 t  
ORIGIN

Query Match 36.1%; Score 25.6; DB 9; Length 282;  
Best Local Similarity 66.1%; Pred. No. 1e+03;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 1 GCACCTGTCGACCCATCGGTCGACCGACCGACCTGGCGGAGACAGC 56  
47 GCACACTGCCCTTCCAGGTGGGTGAAGCCGACCGACGAGGAGGATGC 102

RESULT 32  
LOCUS AT1206415 295 bp mRNA linear EST 29-NOV-1998  
DEFINITION q922g08.x1 NCI-CGAP\_Kid3 Homo sapiens cDNA clone IMAGE:1761854 3',  
mRNA sequence.  
ACCESSION AT1206415  
VERSION AT1206415.1 GI:3765087  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 295)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.lnl.gov/bdrrp/image/image.html](http://www.bio.lnl.gov/bdrrp/image/image.html)  
Insert Length: 379 Std Error: 0.00  
Seq primer: -40UP from Gibco.  
Location/Qualifiers  
1. 295  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1761854"  
/clone\_lib="NCI-CGAP\_Kid3"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer,  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pT7T3 vector. mRNA  
source: 2 pooled kidneys. Library went through one round  
of normalization. Library constructed by Bento Soares and  
M. Fatima Bonaldi."



JOURNAL  
COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bdrrp/image/image.html  
Insert Length: 512 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 286.  
Location/Qualifiers  
1.301  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2312266"  
/clone\_lib="NCI\_CGAP\_Pr28"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI\_CGAP\_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 63 a 89 c 98 g 51 t  
ORIGIN  
Query Match 36.1%; Score 25.6; DB 9; Length 301;  
Best Local Similarity 66.1%; Pred. No. 1e+03;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 1 GCACCTGCCAGCCATGCCGTCCGACCGACCGACTGGCGGAGAGACAGC 56  
DB 50 GCACACTGCCCTTCCAGGTGGGTGAACCCGACGACGAGGAGAGATGTC 105  
RESULT 36  
AM514612 330 bp mRNA linear EST 03-MAR-2000  
LOCUS xus6g11.x1 NCI\_CGAP\_Ut2 Homo sapiens cDNA clone IMAGE:2808644 3',  
DEFINITION mRNA sequence.  
ACCESSION AM514612  
KEYWORDS AM514612.1 GI:7152694  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 330)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bdrrp/image/image.html  
Insert Length: 512 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 319.  
JOURNAL  
COMMENT

FEATURES  
Source Location/Qualifiers  
1.330  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2808644"  
/clone\_lib="NCI\_CGAP\_Ut2"  
/tissue\_type="moderately differentiated endometrial adenocarcinoma, 3 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: PCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"  
BASE COUNT 70 a 97 c 104 g 58 t 1 others  
ORIGIN  
Query Match 36.1%; Score 25.6; DB 9; Length 330;  
Best Local Similarity 66.1%; Pred. No. 1.1e+03;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 1 GCACCTGCCAGCCATGCCGTCCGACCGACCGACTGGCGGAGAGACAGC 56  
DB 57 GCACACTGCCCTTCCAGGTGGGTGAACCCGACGACGAGGAGAGATGTC 112  
RESULT 37  
A1358269 333 bp mRNA linear EST 15-FEB-1999  
LOCUS qw19g07.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:1991580 3',  
DEFINITION mRNA sequence.  
ACCESSION A1358269  
KEYWORDS A1358269.1 GI:4109890  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 333)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bdrrp/image/image.html  
Insert Length: 2174 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 286.  
Location/Qualifiers  
1.333  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1991580"  
/clone\_lib="NCI\_CGAP\_Ut3"  
/tissue\_type="poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: PCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"  
BASE COUNT 67 a 98 c 110 g 58 t  
ORIGIN  
Query Match 36.1%; Score 25.6; DB 9; Length 333;  
Best Local Similarity 66.1%; Pred. No. 1.1e+03;

[illegible]





Db 49 GCACACTGCCCTTCCAGGTGGGTGAAGCCAGCAGGAGGAGGAGGATGC 104  
RESULT 43  
LOCUS A1392737 390 bp mRNA linear EST 30-MAR-1999  
DEFINITION t923611.x1 NCI\_CGAP\_CLL1 Homo sapiens cDNA clone IMAGE:2109644 3',  
mRNA sequence.  
ACCESSION A1392737  
VERSION A1392737.1 GI:4222284  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 390)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,  
M.D., Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution Information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbfp/image/image.html  
Insert Length: 873 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 325.  
Location/Qualifiers  
1. 390  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2109644"  
/clone\_lib="NCI\_CGAP\_CLL1"  
/issue\_type="B-cell, chronic lymphocytic leukemia"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTTCACATCTGAAAGTGGAGCGGCGCATGCTTTTCTTTTCTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 79 a 128 c 121 g 62 t  
ORIGIN  
Query Match 36.1%; Score 25.6; DB 9; Length 390;  
Best Local Similarity 66.1%; Pred. No. 1,le+03;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
OY 1 GCACACTGTCGACCATGCGTCCAGCCGACCGACCTGGCGGAGACAGCAGC 56  
Db 52 GCACACTGCCCTTCCAGGTGGGTGAAGCCAGCAGGAGGAGGAGGATGC 107  
RESULT 44  
LOCUS A1139703 395 bp mRNA linear EST 27-OCT-1998  
DEFINITION qc20d03.x1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone  
IMAGE:1710149 3', mRNA sequence.  
ACCESSION A1139703  
VERSION A1139703.1 GI:3645675  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 395)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royally-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 619 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 330.  
Location/Qualifiers  
1. 395  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1710149"  
/clone\_lib="Soares\_fetal\_heart\_NbHH19W"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: heart; Vector: pT73D (Pharmacia) with a  
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTCACATCTGAAAGTGGAGCGGCGCATGCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M. Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NBHL19W."  
BASE COUNT 79 a 129 c 121 g 66 t  
ORIGIN  
Query Match 36.1%; Score 25.6; DB 9; Length 395;  
Best Local Similarity 66.1%; Pred. No. 1,le+03;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
OY 1 GCACACTGTCGACCATGCGTCCAGCCGACCGACCTGGCGGAGACAGCAGC 56  
Db 55 GCACACTGCCCTTCCAGGTGGGTGAAGCCAGCAGGAGGAGGAGGATGC 110  
RESULT 45  
LOCUS BM129442 395 bp mRNA linear EST 27-NOV-2001  
DEFINITION if22d06.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens  
CDNA 3', mRNA sequence.  
ACCESSION BM129442  
VERSION BM129442.1 GI:17123994  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 395)  
AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,  
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
Hillier, L., Maria, M., Pape, D., Wylie, F., Martin, J., Blistein, A.,  
Schmitt, A., Theising, B., Rittler, E., Ronko, I., Bennett, J., Cardenas  
, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T.,  
Jackson, Y., and Bowers, Y.  
TITLE Endocrine Pancreas Consortium  
JOURNAL Unpublished (2000)  
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138



```

source
1. .414
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:714180"
/clone_id="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="Ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pTV3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAACTGGAGCGCGCGCGGTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTV3 vector (Pharmacia). Library constructed by Bento Soares and M.Fátima Bonaldo."

BASE COUNT      81 a      138 c      130 g      65 t

Query Match      36.1%; Score 25.6; DB 9; Length 414;
Best Local Similarity 66.1%; Pred. No. 1.1e+03;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Oy      1  GCAACCTGCGACCCATGCGATCGGACCCGACGACCTGGCGCGGACAGACAGC 56
Db      41  GCACAGTCCCTCCCGAGGTGGGTGAGCCAGCGACGAGGAGAGAGATCC 96

RESULT 48
BF435851
LOCUS      BF435851
DEFINITION      nab42601.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3268776 3', mRNA sequence.
ACCESSION      BF435851
VERSION        BF435851.1
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 442)
NCI-CCAG http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNT; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Seq primer: -40UP from Glibco.
Location/Qualifiers
1. .442
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/lab_host="DH10B"
/note="Organ: pooled; Vector: pTV3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares Nb2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2H8-9W pool 1: 758280-760583, 772104-774407 Soares NbHFA pool 1: 304776-306311, 320136-322823, 326280-32663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtractive by Bento

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	BASE COUNT	82 a	146 c	142 g	72 t	
	ORIGIN					
	Query Match	36.1%	Score 25.6;	DB 10;	Length 442;	
	Best Local Similarity	66.1%;	Pred. No. 1.le+03;	Mismatches 19;	Indels 0;	Gaps 0;
	Matches 37;	Conservative	0;	Mismatches	19;	Indels 0;
OY	1 GCACCTGTCCGACCATTGCCTCGAAGCCGACCGACTGGCGGGAGACAGACC	56				
Db	45 GCACACTGCCCTTCCACGATGGGGTGGAAGCCAGCAGCACGAGGAGGACAGAGCATGC	100				
RESULT 49						
W02503	W02503	444 bp	mRNA	linear	EST 18-APR-1996	
LOCUS	zcf4g01.s1 Soares fetal heart NbH19W Homo sapiens cDNA clone					
DEFINITION	IMAGE:327120 3', mRNA sequence.					
ACCESSION	W02503					
VERSION	W02503.1 GI:1274694					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 444) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston , R., Williamson,A., Wobldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995)					
TITLE	The WashU-Merck EST Project					
JOURNAL	Unpublished (1995)					
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET High quality sequence stop: 280.					
FEATURES						
Source	Location/Qualifiers					
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	/sex="unknown"					
	/dev_stage="19 weeks"					
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	/note="Organ: heart; Vector: pRT73D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I... oligo(dT) primer [5' TGTTACCAATCTGAATGGAGCGCGCCGCAATCTTTTTTTTTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a cot = 5. Library constructed by M.Felima Bernaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbH19W."					
BASE COUNT	84 a	140 c	143 g	75 t	2 others	
ORIGIN						
Query Match	36.1%;	Score 25.6;	DB 10;	Length 444;		
Best Local Similarity	66.1%;	Pred. No. 1.le+03;	Mismatches 19;	Indels 0;	Gaps 0;	
Matches 37;	Conservative	0;	Mismatches	19;	Indels 0;	Gaps 0;
Y	1 GCACCTTCGACCCATGCGGTCCGAAGCCGACCGACTGGCGGGAGACAGACC	56				

Db 39 GCACACTGCCCTTCCAGGTGGGTGAAGCCAGCCAGACGAGGAGGAGGATGC 94

## RESULT 50

LOCUS

AI978690

DEFINITION AI978690 457 bp mRNA linear EST 08-MAR-2000  
 w158c12.x1 NCI\_CGAP-Ut1 Homo sapiens cDNA clone IMAGE:2491894 3',  
 mRNA sequence.

ACCESSION

AI978690

VERSION AI978690.1 GI:5803720  
 EST.

KEYWORDS

human.

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 457)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL

Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

COMMENT

CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bdrrp/image/image.html](http://www-bio.llnl.gov/bdrrp/image/image.html)  
 Insert Length: 1599 Std Error: 0.00  
 Seq primer: -400P from Gibco

High quality sequence stop: 352.  
 Location/Qualifiers

## FEATURES

1..457

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/clone\_image="IMAGE:2491894"

/clone\_id="NCI\_CGAP-Ut1"

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/lab\_host="DH10B"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.75 kb. Life Technologies catalog #:  
 11538-014"

BASE COUNT

88 a 150 c 150 g 68 t 1 others

ORIGIN

Query Match

36.1% Score 25.6; DB 9; Length 457;

Best Local Similarity 66.1% Pred. No. 1.1e+03;

Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GCACACTGTCGACCCATCGCGTCCGAACCGCACCGACTGGGGGAGAGAGACAGC 56  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 30 GCACACTGCCCTTCCAGGTGGGTGAAGCCAGCCAGACGAGGAGGAGGATGC 85  
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